

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 16:33:30 ; Search time 3423 Seconds
(without alignments)
15968.534 Million cell updates/sec

Title: US-10-602-166-2

Perfect score: 1436

Sequence: 1 cattcagaatcatctccagc.....tatcagtggtccaactgy 1436

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_hic: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307.2	21.4	376	9	CL921501 OA_ABA002
2	130.8	9.1	612	9	CL835542 OR_CBA005
3	126	8.8	784	9	CL852571 OR_CBA008
4	126	8.8	829	9	CL855333 OR_CBA008
5	124	8.6	840	9	CL728092 OR_CBA005
6	123.6	8.6	781	9	CL783664 OR_BB010
7	119.8	8.3	486	9	CL811645 OR_CBA002
8	107.8	7.5	665	9	CL708436 OR_BB002
9	107.8	7.5	820	9	CL854157 OR_CBA008
10	107.8	7.5	824	9	CL782578 OR_BB009
11	105.2	7.3	784	9	CL746481 OR_CBA008
12	104.6	7.3	707	9	CL807668 OR_CBA002
13	104.6	7.3	757	9	CL843536 OR_CBA007
14	104	7.2	590	8	AQ328957 nbxb00441
15	100.6	7.0	431	9	CG206879 TOS0501 T
16	99.6	6.9	651	9	CW508204 OP_Ba000
17	99	6.9	387	8	AQ912524 nbeb00371
18	99	6.9	845	8	AZ045366 nbcb0080N
19	98.8	6.9	771	9	CL753477 OR_BB012
20	98.4	6.9	754	9	CL858870 OR_CBA008
21	97	6.8	723	9	CL817465 OR_CBA003
22	94.4	6.6	491	9	CL739488 OR_BB007
23	93.4	6.5	365	6	C72467 C72467 Rice
24	92.2	6.4	561	9	CL752715 OR_BB011

25	91.4	6.4	280	6	C71788	C71788 C71788 Rice
26	91.2	6.4	642	8	AQ578656	AQ578656 nbxb0093C
27	90.2	6.3	624	9	CL790230	CL790230 OR_BB010
28	90.2	6.3	640	9	CL749018	CL749018 OR_BB011
29	90.2	6.3	774	9	CL612072	CL612072 OR_BB000
30	90	6.3	562	9	CL629198	CL629198 OR_BB002
31	88.4	6.2	754	8	AQ840531	AQ840531 nbxb0063P
32	86.2	6.0	699	9	CL858276	CL858276 OR_CBA008
33	86.2	6.0	773	9	CL736927	CL736927 OR_BB007
34	86	6.0	742	9	CL627803	CL627803 OR_BB002
35	84.6	5.9	738	9	CL753761	CL753761 OR_BB012
36	83.2	5.8	789	9	CL768364	CL768364 OR_BB014
37	82.8	5.8	621	9	CW538474	CW538474 OP_Ba005
38	82.6	5.8	617	9	AG211983	AG211983 Oryza sat
39	81.2	5.7	745	9	CL853543	CL853543 OR_CBA008
40	81	5.6	336	9	CL838261	CL838261 OR_CBA006
41	81	5.6	576	9	AG212556	AG212556 Oryza sat
42	81	5.6	756	9	CL859905	CL859905 OR_CBA009
43	80.6	5.6	677	9	CL772037	CL772037 OR_BB008
44	80	5.6	490	9	AB156569	AB156569 Oryza sat
45	80	5.6	685	9	AG021430	AG021430 Oryza sat

ALIGNMENTS

RESULT 1
LOCUS CL921501/c 376 bp DNA linear GSS 14-SEP-2004
DEFINITION OA_ABA0026D24.r OA_ABA Oryza australiensis genomic clone
VERSION OA_ABA0026D24 3', genomic survey sequence.
CL921501
CL921501.1 GI:52037176
GSS.

SOURCE
ORGANISM Oryza australiensis
Oryza australiensis

REFERENCE
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0026 row: D column: 24
Seq primer: CAC TCA TTA GGC ACC CCA
Classes: BAC ends.

FEATURES
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/db_xref="taxon:4532"
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/tissue_type="young leaves"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OA_ABA"
/note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN

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Best Local Similarity 94.1%; Pred. No. 2e-66;
Matches 354; Conservative 0; Mismatches 13; Indels 9; Gaps 3;

Oy 510 AATGTCATGATCTGCATGCATCGCCAGATTATATTCTCATTCTTTCTTCC 569
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Db 376 AATGTCCATGATCTGCATGCATCGCCAGATTATATTCTCATTCTTTCTTCC 317
Oy 570 TATGCTCTCTAGTC-----GTCGTGTTGGAGCTTAAATTATGAAAAGCAGCTGCTG 622
|||
Db 316 TATGCTCTCTAGTCCTTCTATGCTCTGTAGGAGCTTAAATTCCGAGAAACAGCTGCTG 257
Oy 623 AGAAGCTAGCTGTGAGAACTGGAATTGAGTTGACTTCACTTCTCCAGATTCTAC 682
|||
Db 256 AGAAGTAGCTGTGAGAACTGGAATTGAGTTGACTTCACTTCTCCAGATTCTAC 198
Oy 683 AATTACAGATTCTTATATTAGTAAAGCTGACTGTTT-GGGAGCTTCTGTACGCC 741
|||
Db 197 AATTACAGATTCTTAGAAATTAGTAAAGCTGACTGTTTGGGAGCTTCTGTACGCC 138
Oy 742 GGAGATTCTGTGAGAAAGCTGCAGCTGCTAGAAAGCTTCCCAACAGACCCCTAGTTGTAC 801
|||
Db 137 GGAGATTCTGGGAGAAAGCTGCACACTGCTAGAAAGCTTCCCAACAGACCCCTAGTTGTAC 78
Oy 802 TCTAGCTGATGCATTCACCTTATTTATATACACCTTGCTCTAGCTTATCAAAACGTAG 861
|||
Db 77 TCCAGCTGATGCATTCACCTTATTTATATGCACTTGCTCTAGCTTATCAAAACGTAG 18
Oy 862 CCAAGACTTGAATTTT 877
|||
Db 17 CCAAGACTTGAATTTT 2

RESULT 2
CL835542/c 612 bp DNA linear GSS 09-AUG-2004
LOCUS OR_CBA0059F08.f OR_CBA Oryza rufipogon genomic clone OR_CBA0059F08
DEFINITION 5', genomic survey sequence.
ACCESSION CL835542
VERSION CL835542.1 GI:51081152
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 612)
Kim,H., Yu,Y., Wisnietki,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jecty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0059 row: F column: 08
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES
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Location/Qualifiers
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBA0059F08"
/issue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
dirk treated 36 hrs before harvest"

ORIGIN
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Best Local Similarity 75.2%; Pred. No. 7.9e-22;
Matches 191; Conservative 0; Mismatches 57; Indels 6; Gaps 2;
Oy 581 GTGCTGTGTTGGAGCTTAAATATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAGA 640
|||
Db 433 GGCGTGTGTTGGGAGATTAGATTCCGAGAAGCTGCTGTGAGAAGCTAGCTGTGAGA 374
Oy 641 ATCTGAAGATTG---AGTTCTACGTTCTATCTTCCAGATTCTACATTACAGATTCTT 696
|||
Db 373 ATCTAGAGAAGCTGGGAAAGCTTCTAGTTCAATTGTCAGATTCTACAGATTCTC 314
Oy 697 ATATTTAGTTAAGTAAAGCTGACTGTTT--GGAGCTTCTGTACAGCCGAGATTCTGTGA 754
|||
Db 313 AGAATCTGGGTAAAAAGTTGACTGTTTGGGGAGCTTCTGGCAACTGGAGATTCTAGGA 254
Oy 755 GAAGCTCAGCTGCTAGAAAGCTTCCCAACAGACCCCTAGTTGTACTCTAGCTGATCGA 814
|||
Db 253 GAAGCTCAGCTGCTAGAAAGCTTCCCAACAGACCCCTTAGGCTTGTGCGCAGTGAGC 194
Oy 815 TTCACTCTATTTTA 828
|||
Db 193 TTTTCCAGCTTATA 180

RESULT 3
CL852571 784 bp DNA linear GSS 16-AUG-2004
LOCUS OR_CBA0081H21.f OR_CBA Oryza rufipogon genomic clone OR_CBA0081H21
DEFINITION 5', genomic survey sequence.
ACCESSION CL852571
VERSION CL852571.1 GI:51256951
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 784)
Kim,H., Yu,Y., Wisnietki,M., Yost,D., Stum,D., Rao,K., Luo,M.,
Jecty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
Wing,R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0081 row: H column: 21
Seq primer: TAA TAC GAC TCA CTA TAG GG
Classes: BAC ends.

FEATURES
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Location/Qualifiers
/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBA0081H21"
/issue_type="young leaves"
/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBA"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
dirk treated 36 hrs before harvest"

ORIGIN

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Best Local Similarity 80.1%; Pred. No. 1.4e-20;
Matches 173; Conservative 0; Mismatches 40; Indels 3; Gaps 2;

QY 581 GTCGCTGTTGGGAGCTTAAATATATGAAGCAGCTGCTGAGAAGCTAGCTGTGAGA 640
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 391 GACCTGTTGGGGAGGTTAGATTCTGAAAAGCAGCCGCTAGAAGCTAGCTGTGAGA 450
QY 641 ATCTGAGAATTTGAGTTCTACGTTCAATTCPCAGATTCTACAATTACAGATTCTTATA 700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 451 AACCCAGC--TTCTGGCTTCTAGTTCATTCTTAGATTCTACAACCTACAGATTCTTAGAA 508
QY 701 TTTAGGTAAAAAGCTGGAAGCTGTTGGG-AGCTTCTGTCAAGCCGAGATTCTGTAGAAGC 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 509 TCTAGGTAAATGCTGGAAGCTGTTGGGAAGCTTCTGGCAACTGAGAGATTCTAGAGAAGC 568
QY 760 TGCAGCTGCTAGAAGCTTCCCCAACAAGACCCCTAG 795
DB 569 TGCAGTTGCTAGAAGCTCCCCCAATAGGCCCTTAG 604

RESULT 4
LOCUS CL855333 829 bp DNA linear GSS 16-AUG-2004
DEFINITION OR_CBa0085C07.f OR_CBa Oryza rufipogon genomic clone OR_CBa0085C07
5', genomic survey sequence.
ACCESSION CL855333
VERSION CL855333.1 GI:51263573
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 829)
AUTHORS Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
          Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
          Wing,R.
TITLE OMAP project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
          Arizona Genomics Institute
          University of Arizona
          Forbes Building Room 303, Tucson, AZ 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0085 row: C column: 07
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

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         /dev_stage="2 week old seedlings"
         /lab_host="DH10B T1 phage resistant"
         /clone_lib="OR_CBa"
         /note="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII;
         dtk treated 36 hrs before harvest"

ORIGIN
Query Match      8.8%; Score 126; DB 9; Length 829;
Best Local Similarity 80.1%; Pred. No. 1.4e-20;
Matches 173; Conservative 0; Mismatches 40; Indels 3; Gaps 2;

QY 581 GTCGCTGTTGGGAGCTTAAATATATGAAGCAGCTGCTGAGAAGCTAGCTGTGAGA 640
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DB 393 GACCTGTTGGGGAGGTTAAGTTCTGAAAAGCAGCCGCTAGAAGCTAGCTGTGAGA 452
QY 641 ATCTGAGAATTTGAGTTCTACGTTCAATTCCTCCAGATTCTACAATTACAGATTCTTATA 700
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 453 AACCCAGC--TTCTGGCTTCTAGTTCATTCTTAGATTCTACAACCTACAGATTCTTAGAA 510
QY 701 TTTAGGTAAAAAGCTGGAAGCTGTTGGG-AGCTTCTGTCAAGCCGAGATTCTGTAGAAGC 759
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 511 TCTAGGTAAATGCTGGAAGCTGTTGGGAAGCTTCTGGCAACTGGAGATTCTAGAGAAGC 570
QY 760 TGCAGCTGCTAGAAGCTTCCCCAACAAGACCCCTAG 795
DB 571 TGCAGTTGCTAGAAGCTCCCCCAATAGGCCCTTAG 606

RESULT 5
LOCUS CL728092 840 bp DNA linear GSS 27-JUL-2004
DEFINITION OR_BBa0059A19.f OR_BBa Oryza rufipogon genomic clone OR_BBa0059A19
5', genomic survey sequence.
ACCESSION CL728092
VERSION CL728092.1 GI:50662448
KEYWORDS GSS.
SOURCE Oryza rufipogon
ORGANISM Oryza rufipogon
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 840)
AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
          Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
TITLE OMAP Project
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
          Arizona Genomics Institute
          University of Arizona
          Forbes Building Room 303, Tucson, AZ 85721-0036, USA
          Tel: 520 626 9595
          Fax: 520 621 1259
          Email: http://genome.arizona.edu
PCR PRIMERS
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
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Class: BAC ends.

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         /lab_host="DH10B-T1 phage resistant"
         /clone_lib="OR_BBa"
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ORIGIN
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Best Local Similarity 84.1%; Pred. No. 4.4e-20;
Matches 175; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

QY 589 TTTGGAGCTTAAATATATGAAGCAGCTGCTGAGAAGCTAGCTGTGAGAATCTGAAG 648
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DB 436 TTGGGAGGTTAAGATTCTGAAAAGCAGCTGCTAAGAGCTAGCTGTGAGAAAC-CCAG 494
QY 649 AATTGAGTTCTACGTTCAATTCCTCCAGATTCTACAATTACAGATTCTTATAATTAGGTA 708
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 495 CTTCTGAACTTCTA-GTTATTTTCTAGATTCTACAACCTACAGATTCTTAGAATATAGGTA 553
QY 709 AAAAGCTGACTGTTGGG-AGCTTCTGTCAAGCCGAGATTCTGTAGAAGCTGACGCTG 767
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 554 AAAAGCTGACTGTTTGGGAAGCTTCTAGCACTGAAGATTCTAGGAGAAGCTGCAGTTG 613

Qy 768 CTAGAAGCTTCCCCAAACAGACCCCTAG 795

Db 614 CTAGAAGCTCCCCAAATAGGCCCTTAG 641

RESULT 6
CL783664

LOCUS CL783664 781 bp DNA linear GSS 30-JUL-2004

DEFINITION OR_BBa0100G05.f OR_BBa Oryza rufipogon genomic clone OR_BBa0100G05 5', genomic survey sequence.

ACCESSION CL783664

VERSION CL783664.1 GI:50863315

KEYWORDS GSS.

SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 781)

AUTHORS Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing
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University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0100 row: G column: 05
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.

FEATURES
Location/Qualifiers
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/clone_lib="OR_BBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

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Query Match 8.6%; Score 123.6; DB 9; Length 781;
Best Local Similarity 84.5%; Pred. No. 5.5e-20;
Matches 174; Conservative 0; Mismatches 29; Indels 3; Gaps 3;

Qy 589 TTTGGAGCTTAAATATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAATCTGAAG 648

Db 436 TTGGGAGGTTAAGATTCTGAAAGCAGCTGCTAAGAAGCTAGCTGTGAGAAGC-CCAG 494

Qy 649 AATTGAGTTCTACGTTTCATCTCCAGATTCTACAATTACAGATTCTTATAATTAGTA 708

Db 495 CTTCTGACTTCTA-GTTATTCTTAGATTCTACAATTCTTGAATATAGGTA 553

Qy 709 AAAAGCTGACTGTTGGG-AGCTTCTGTCAACCCGAGATTCTGTGAGAAGCTGCAGCTG 767

Db 554 AAAAGCTGACTGTTGGGAAGCTTCTAGCAACTGAAGATTCTAGGAGAAGCTGCAGTTG 613

Qy 768 CTAGAAGCTTCCCCAAACAGACCCCT 793

Db 614 CTAGAAGCTCCCCAAATAGGCCCT 639

RESULT 7

CL811645

LOCUS CL811645 486 bp DNA linear GSS 09-AUG-2004

DEFINITION OR_CBa0027D24.r OR_CBa Oryza rufipogon genomic clone OR_CBa0027D24 3', genomic survey sequence.

ACCESSION CL811645

VERSION CL811645.1 GI:51051839

KEYWORDS GSS.

SOURCE Oryza rufipogon

ORGANISM Oryza rufipogon

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. 1 (bases 1 to 486)

AUTHORS Kim,H., Yu,Y., Wisnorski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.

TITLE OMAP Project

JOURNAL Unpublished (2004)

COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu

PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0027 row: D column: 24
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.

FEATURES
Location/Qualifiers
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/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
/clone="OR_CBa0027D24"
/tissue_type="young leaves"
/dev stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"

ORIGIN

Query Match 8.3%; Score 119.8; DB 9; Length 486;
Best Local Similarity 72.1%; Pred. No. 4.5e-19;
Matches 191; Conservative 0; Mismatches 57; Indels 17; Gaps 2;

Qy 581 GTGCTCTGTTGGAGCTTAAATATGAAAGCAGCTGCTGAGAAGCTAGCTGTGAGA 640

Db 8 GGCTGTTTGGGAGCTTAAGATTTTGAGAAGCAGCTGCTGAGAAGCTAGCCGGTGAGA 67

Qy 641 ATCTGAAGATTGA-----GTTCTACGTTTCATTTCTCAGATTCTACAAT 685

Db 68 ATCTGAGAAGCTGGAACCACAGCTTCTGCTTCTAGTTCAATTTTCAGATTCTACAAC 127

Qy 686 TACAGATTCTTATAATTAGTAAGTAAGAGCTGAGCTGTT--GGAGCTTCTGTACGCCG 743

Db 128 TACAGATTCTCAGAAATCTGGGTAAGGCTGAGCTGTTTGGGGAGCTTCTGACAACTGG 187

Qy 744 AGATTCTGTGAGAAGCTGCAGCTGCTAGAAAGCTTCCCAACAGACCCCTAGTTGTAATC 803

Db 188 AGATTCTAGTAGAAGCTACAGCTGCTAGAAAGCTTCCCAACAGGCCCATATGACAACCT 247

Qy 804 TAGCTGATCGATTCACTTAATTTTA 828

Db 248 ACTCTCCTCTTTGGGCTGCAGTTAA 272

RESULT 8
CL708436

LOCUS CL708436 665 bp DNA linear GSS 26-JUL-2004

DEFINITION	OR_BBa0029A21.r OR_BBa Oryza rufipogon genomic clone OR_BBa0029A21 3', genomic survey sequence.						
ACCESSION	CU708436						
VERSION	CU708436.1 GI:50595474						
KEYWORDS	GSS.						
SOURCE	Oryza rufipogon						
ORGANISM	Oryza rufipogon						
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza. 1 (bases 1 to 665)						
AUTHORS	Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.						
TITLE	OMAP Project						
JOURNAL	Unpublished (2004)						
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: http://genome.arizona.edu PCR Primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Insert Length: 161 Std Error: 0.00 Plate: 0029 row: A column: 21 Seq primer: CAC TCA TTA GGC ACC CCA Class: BAC ends.						
FEATURES	location/Qualifiers						
source	1..665						
	/organism="Oryza rufipogon"						
	/mol_type="genomic DNA"						
	/db_xref="taxon:4529"						
	/clone="OR_BBa0029A21"						
	/tissue_type="young leaves"						
	/lab_host="DH10B-T1 phage resistant"						
	/clone_1lb="OR_BBa"						
	/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"						
ORIGIN							
Query Match	7.5%;	Score	107.8;	DB 9;	Length	665;	
Best Local Similarity	73.0%;	Pred. No.	5.2e-16;				
Matches	173;	Conservative	0;	Mismatches	47;	Indels	17; Gaps 2;
OY	580 AGTCGCTGTGGAGCTTAAATTATGAAGAAGCAGCTGCTGAAGCTAGCTGTGAG	639					
Db	355 AGCCCTGTTAGGGAGCTTGAGATTCTAAGAAGCTGCTGCGTAGAAGCTACTGTGAG	414					
OY	640 AATCTGAAGAATTGAGT-----TCTACGTTCA TTCTCCAGATTCTACA	684					
Db	415 AATCTGA AAAAGCTGAGAAA CCTAGCTTCTGCGTTCTAGTTCATTTTACAGATTCTATA	474					
OY	685 TTACAGATTCTTATAATTAGGTA AAAAGCTGAGCTGTT--GGAGCTTCTGTACGCC	742					
Db	475 CTACATATTTTCA GAATCTAAGTAATAATAGCTGAGCTGTTGGGGAGGTTTCTGCCAACTG	534					
OY	743 GAGATTCTGTGAAGAAGCTGCAAGCTCTAGAAAGCTTCCCACAA CAGACCCTAGTTGT	799					
Db	535 AAGATTCTAGAGAAGCTGCAAGCTGTTAGAAACTCCACCAA CAGACCCTTAACAGT	591					
RESULT 9							
LOCUS	CU854157	820 bp	DNA	linear	GSS	16-AUG-2004	
DEFINITION	OR_CBA0083J07.f OR_CBA Oryza rufipogon genomic clone OR_CBA0083J07 5', genomic survey sequence.						
ACCESSION	CU854157						
VERSION	CU854157.1 GI:51260708						
KEYWORDS	GSS.						
SOURCE	Oryza rufipogon						
ORGANISM	Oryza rufipogon						
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						

REFERENCE	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
AUTHORS	1 (bases 1 to 820) Kim,H., Yu,Y., Wissotski,M., Yost,D., Stum,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and wing,R.				
TITLE	OMAP project				
JOURNAL	Unpublished (2004)				
COMMENT	Contact: Rod A. Wing Arizona Genomics Institute University of Arizona Forbes Building Room 303, Tucson, AZ 85721-0036, USA Tel: 520 626 9595 Fax: 520 621 1259 Email: http://genome.arizona.edu PCR Primers FORWARD: TAA TAC GAC TCA CTA TAG GG BACKWARD: CAC TCA TTA GGC ACC CCA Plate: 0083 row: J column: 07 Seq primer: TAA TAC GAC TCA CTA TAG GG Class: BAC ends.				
FEATURES	Location/Qualifiers				
SOURCE	1. 820 /organism="Oryza rufipogon" /mol_type="genomic DNA" /db_xref="taxon:4529" /clone="OR_CBa0083J07" /tissue_type="young leaves" /dev_stage="2 week old seedlings" /lab_host="DH10B T1 phage resistant" /clone_lib="OR_CBa" /note="Vector: pGIBACL1; Site_1: HindIII; Site_2: HindIII; dkf treated 36 hrs before harvest"				
ORIGIN					
Query Match	7.5%;	Score 107.8;	DB 9;	Length 820;	
Best Local Similarity	73.0%;	Pred. No. 5.4e-16;			
Matches 173;	Conservative 0;	Mismatches 47;	Indels 17;	Gaps 2;	
OY	580	AGTCGCTGTTGGGAGCTTAAATTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAG	639		
Db	334	AGCCCTGTTAGGGAGCTTGAGATTCTAAGAAGCTGCTGAGAAGCTACTGTGTAG	393		
OY	640	AATCTGAAGAATTGAGT-----TCTACGTTCAATCTCCAGATTCTACAA	684		
Db	394	AATCTGAAAAGCTGAGAAACCTAGCTTCTGCTTCTAGTTCATTTACAGATTCTATAA	453		
OY	685	TTACAGATTCTTAATTTAGGTAAAGCTGACGTGTTT--GGAGCTTCTGTACGCCG	742		
Db	454	CTACATATTTTCAGATCTAAGTAATAAGCTGACGTGTTGGGGAGTTCTGTCCAAC	513		
OY	743	GAGATCTGTGAGAGAGCTGCAGCTGCTAGAGCTTCCCAACACAGACCCCTAGTTGT	799		
Db	514	AAGATTCTAGGAGAGCTGCAGCTGTTAGAAACTCCACCAACAGACCCCTTAACAGT	570		
RESULT 10					
LOCUS	CL782578	824 bp	DNA	linear	GSS 30-JUL-2004
DEFINITION	OR_BBa0098L11.f OR_BBa Oryza rufipogon genomic clone OR_BBa0098L11				
ACCESSION	5', genomic survey sequence.				
VERSION	CL782578				
KEYWORDS	CL782578.1 GI:50862174				
SOURCE	GSS.				
ORGANISM	Oryza rufipogon				
	Oryza rufipogon				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.				
REFERENCE	1 (bases 1 to 824) Kim,H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and wing,R.				
AUTHORS	OMAP Project				
TITLE					


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source
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/organism="Oryza rufipogon"
/mol_type="genomic DNA"
/db_xref="taxon:4529"
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/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
/clone_lib="OR_CBa"
/notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII;
dkr treated 36 hrs before harvest"

ORIGIN

Query Match      7.3%; Score 104.6; DB 9; Length 707;
Best Local Similarity 72.5%; Pred. No. 3.4e-15;
Matches 169; Conservative 0; Mismatches 49; Indels 15; Gaps 2;

OY 579 TAGTCGTCGTTGGGAGCTTAAATATGAAAAAGCAGCTGCTGAGAGCTAGCTGTGA 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 TAGGCGCTGTTAGGGGAAGCTTAAATCTGAGAAAAGCTGCTAAGAGCTAGCTGTGA 355
OY 639 GAATCTGAAGAATTGA-----GTTCTACGTTCAATCTCCAGATTCTACAA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 356 GAATTGGAGAAAGCTGTAAACCAGCTTCTGCTTCTAGCTCATTTTCAGATTCTACAA 415
OY 685 TTACAGATTCTTATAATTAGTAAAGCTGGAAGCTGTTG-GGAGCTTCTGCAGCCGG 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 416 TTACATATTCTCAGATCTAGATATAAAGCTAGACTGTTTGAGGAGCTTTTAACAATAA 475
OY 744 AGATTCGTGAGAAAGCTGCAGCTGCTAGAGCTTCCCAACAGACCCCTAGT 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 476 AAATTCTAAAGAAGAACTGCAGCTGCTAGAGCTCTCCAAAACATACCCGTGT 528
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RESULT 13
LOCUS      CL843536              757 bp    DNA        linear    GSS 09-AUG-2004
DEFINITION OR_CBa0072P12.r OR_CBa Oryza rufipogon genomic clone OR_CBa0072P12
3', genomic survey sequence.
ACCESSION  CL843536
VERSION    CL843536.1 GI:51089146
KEYWORDS   GSS.
SOURCE     Oryza rufipogon
ORGANISM   Oryza rufipogon
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 757)
            Kim,H., Yu,Y., Wismotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,
            Jettly,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and
            Wing,R.
TITLE      OMAF project
JOURNAL    Unpublished (2004)
COMMENT    Contact: Rod A. Wing
            Arizona Genomics Institute
            University of Arizona
            Forbes Building Room 303, Tucson, AZ 85721-0036, USA
            Tel: 520 626 9595
            Fax: 520 621 1259
            Email: http://genome.arizona.edu
            PCR Primers
            FORWARD: TAA TAC GAC TCA CTA TAG GG
            BACKWARD: CAC TCA TTA GGC ACC CCA
            Plate: 0072 row: P column: 12
            Seq primer: CAC TCA TTA GGC ACC CCA
            Class: BAC ends.

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location/Qualifiers
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/tissue_type="young leaves"
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/dev_stage="2 week old seedlings"
/lab_host="DH10B T1 phage resistant"
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/notes="Vector: pGIBAC1; Site_1: HindIII; Site_2: HindIII;
dkr treated 36 hrs before harvest"

ORIGIN

Query Match      7.3%; Score 104.6; DB 9; Length 757;
Best Local Similarity 72.5%; Pred. No. 3.4e-15;
Matches 169; Conservative 0; Mismatches 49; Indels 15; Gaps 2;

OY 579 TAGTCGTCGTTGGGAGCTTAAATATGAAAAAGCAGCTGCTGAGAGCTAGCTGTGA 638
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 296 TAGGCGCTGTTAGGGGAAGCTTAAATCTGAGAAAAGCTGCTAAGAGCTAGCTGTGA 355
OY 639 GAATCTGAAGAATTGA-----GTTCTACGTTCAATCTCCAGATTCTACAA 684
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 356 GAATTGGAGAAAGCTGTAAACCAGCTTCTGCTTCTAGCTCATTTTCAGATTCTACAA 415
OY 685 TTACAGATTCTTATAATTAGTAAAGCTGGAAGCTGTTG-GGAGCTTCTGCAGCCGG 743
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 416 TTACATATTCTCAGATCTAGATATAAAGCTAGACTGTTTGAGGAGCTTTTAACAATAA 475
OY 744 AGATTCGTGAGAAAGCTGCAGCTGCTAGAGCTTCCCAACAGACCCCTAGT 796
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 476 AAATTCTAAAGAAGAACTGCAGCTGCTAGAGCTCTCCAAAACATACCCGTGT 528
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RESULT 14
LOCUS      AQ328957/c              590 bp    DNA        linear    GSS 08-JAN-1999
DEFINITION nbxb0044119f CUGI Rice BAC Library Oryza sativa (japonica
cultivar-group) genomic clone nbxb0044119f, genomic survey
sequence.
ACCESSION  AQ328957
VERSION    AQ328957.1 GI:4120807
KEYWORDS   GSS.
SOURCE     Oryza sativa (japonica cultivar-group)
ORGANISM   Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE  1 (bases 1 to 590)
            Wing,R.A. and Dean,R.A.
            A BAC Bnd Sequencing Framework to Sequence the Rice Genome
            Unpublished (1998)
TITLE      Contact: Wing RA
JOURNAL    Clemson University Genomics Institute
COMMENT    Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: twing@clemson.edu
            Seg primer: TAATACGACTCACTATAGGG
            Class: BAC ends
            High quality sequence stop: 324.

FEATURES
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location/Qualifiers
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/notes="Vector: pBeloBAC1; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
```

(Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from *Oryza sativa*, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 Kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."

ORIGIN

Query Match	7.2%	Score 104;	DB 8;	length 590;
Best Local Similarity	76.3%	Pred. No. 4.6e-15;		
Matches 161;	Conservative 0;	Mismatches 31;	Indels 19;	Gaps 2;
QY	592	GGGAGCTTAAATATGATAAAGCAGCTGCTGAGAAAGCTAGCTGTGAGAATCTGAAGAAT	651	
DB	553	GGGAGTTAAGATTCTAAGAAGCAGCTGCTGAGAAAGCTAGCTGTGAGAATCTA-----	500	
QY	652	TTGAGTTACGTTCAATCTCCAGATTCTACAATTACAGATTCTTATAATTAGGTAAA	711	
DB	499	-----GTTCATTTCTCTGATTCTACAACTACAGATTCTCAGAATCTGGATAAA	451	
QY	712	AGCTGACTGTTT--GGGAGCTTCTGTCAAGCCGAGATTCTGTGAGAAGCTGCAGCTGCT	769	
DB	450	ATCTGCACTGTTTGGGGGAGCTTCTGGCAACTGAGATTTTAGAGAAGCTGCAGCTAANT	391	
QY	770	AGAAGCTTCCCCAACAACAGACCCCTAGTTGTA	800	
DB	390	AAAAGCTCCCCCAACAGGCGCTGATTAGGA	360	

RESULT 15
CG206879

CG206879

LOCUS	431 bp	DNA	linear	GSS 21-AUG-2003
CG206879				
TOS0501	TAMU Rice Japonica	Nipponbare BAC Library	(Hind III)	OrYZa

ACCESSION

VERSION CG206879.1 GI:34097940

KEYWORDS

SOURCE

ORGANIS

SOURCE ORGANISM	
Oryza sativa (japonica cultivar-group)	
Oryza sativa (japonica cultivar-group)	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 431)

AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.

TITLE BAC end sequences to close the gaps of a rice physical map at TAMU
JOURNAL Unpublished (2003)

COMMENT

COMMENT

Genomics and Biotechnology

Texas A & M University

TAMU 2474, College Station. TX 77843-2474. USA

Tel: 979 862 4800

Fax: 979 862 4790

ଅନୁସନ୍ଧାନ : ଟ-ଆଇନର ତାଲୁକା କର୍ମୀ

Serial: C 440100:camu:ecu
Sed primer: M13 [universal] Reverse AACAGCTATGACCATG

CJ case: BAC and

class: bnc enus
rich maj:tv sentence ston: 121

high quality sequence block: 431.
Location/Offset: 1461000

FEATURES	LOCATION/QUALITIES
Source	1 431

Source

/organism="Oryza sativa (japonica cultivar-group)"

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ORIGIN

[illegible]

Search completed: September 23, 2005, 19:20:35
Job time : 3430 secs

Job time : 3430 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 17:01:48 ; Search time 714 Seconds
(without alignments)
13447.233 Million cell updates/sec

Title: US-10-602-166-2

Perfect score: 1436

Sequence: 1 cattcagaatcatctccagc.....tatcagtggttcaactcgg 1436

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7400704 seqs, 3343079526 residues

Total number of hits satisfying chosen parameters: 14801408

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1436	100.0	1436	9	US-09-848-696-2
2	1436	100.0	1436	18	US-10-602-166-2
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4	1436	100.0	3003	18	US-10-602-166-1
5	1196	83.3	1196	9	US-09-848-696-3
6	1196	83.3	1196	18	US-10-602-166-3
7	240	16.7	240	9	US-09-848-696-10

8	240	16.7	240	18	US-10-602-166-10	Sequence 10, Appli
9	107.4	7.5	712	19	US-10-437-963-87679	Sequence 87679, A
10	95	6.6	1008	9	US-09-848-696-7	Sequence 7, Appli
11	95	6.6	1008	18	US-10-602-166-7	Sequence 7, Appli
12	93.4	6.5	1054	18	US-10-425-114-30221	Sequence 30221, A
13	93.4	6.5	1250	19	US-10-437-963-72585	Sequence 72585, A
14	90.4	6.3	2000	17	US-10-260-238-2616	Sequence 2616, Ap
15	77.2	5.4	17953	18	US-10-415-058-4	Sequence 4, Appli
16	69.2	4.8	442	19	US-10-437-963-34782	Sequence 34782, A
17	63.4	4.4	5631	19	US-10-437-963-44842	Sequence 44842, A
18	62.2	4.3	451	19	US-10-437-963-89687	Sequence 89687, A
19	61.8	4.3	5682	19	US-10-437-963-44845	Sequence 44845, A
20	58.8	4.1	2000	17	US-10-260-238-1892	Sequence 1892, Ap
21	57.6	4.0	11460	18	US-10-415-058-7	Sequence 7, Appli
22	57.6	4.0	49600	18	US-10-459-262A-4	Sequence 4, Appli
23	57.6	4.0	69300	18	US-10-415-058-6	Sequence 6, Appli
24	57.6	4.0	91552	18	US-10-415-058-5	Sequence 5, Appli
25	56.2	3.9	183	19	US-10-437-963-90519	Sequence 90519, A
26	56.2	3.9	3673778	16	US-10-312-841-1	Sequence 1, Appli
27	55.8	3.9	2000	17	US-10-260-238-1653	Sequence 1653, Ap
28	55.4	3.9	400	19	US-10-437-963-80401	Sequence 80401, A
29	55.4	3.9	835	19	US-10-437-963-97252	Sequence 97252, A
30	51	3.6	395	20	US-10-425-115-45803	Sequence 45803, A
31	51	3.6	603	19	US-10-437-963-44654	Sequence 44654, A
32	50.8	3.5	6239	17	US-10-221-613-28	Sequence 28, Appli
33	50.6	3.5	11534	15	US-10-311-455-316	Sequence 316, App
34	50.4	3.5	6735	15	US-10-311-455-1347	Sequence 1347, Ap
35	50.4	3.5	8056	20	US-10-473-126-386	Sequence 386, App
36	50.2	3.5	438	18	US-10-424-599-125688	Sequence 125688,
37	49.8	3.5	914	19	US-10-767-795-6577	Sequence 6577, Ap
38	49.8	3.5	12763	15	US-10-311-455-276	Sequence 276, App
39	49.6	3.5	5518	20	US-10-473-126-255	Sequence 255, App
40	49.6	3.5	17131	15	US-10-311-455-1025	Sequence 1025, Ap
41	49	3.4	11049	15	US-10-311-455-641	Sequence 641, App
42	49	3.4	11049	18	US-10-240-589C-27	Sequence 27, Appli
43	48.8	3.4	8056	20	US-10-473-126-240	Sequence 240, App
44	48.6	3.4	3673778	16	US-10-312-841-2	Sequence 2, Appli
45	48.4	3.4	456	20	US-10-425-115-132592	Sequence 132592,

ALIGNMENTS

RESULT 1

US-09-848-696-2

; Sequence 2, Application US/09848696

; Patent No. US20010051713A1

; GENERAL INFORMATION:

; APPLICANT: AN, GYN HEUNG

; APPLICANT: JEON, JONG-SEONG

; APPLICANT: CHUNG, YONG-YOON

; APPLICANT: LEE, SI CHUL

; TITLE OF INVENTION: DNA COMPRISING RICE ANTHER-SPECIFIC GENE AND TRANSGENIC PLANT TR

; TITLE OF INVENTION: THEREWITH

; FILE REFERENCE: S-30723A

; CURRENT APPLICATION NUMBER: US/09/848,696

; CURRENT FILING DATE: 2001-05-03

; PRIOR APPLICATION NUMBER: KR 98-46973

; PRIOR FILING DATE: 1998-11-03

; PRIOR APPLICATION NUMBER: KR 98-50126

; PRIOR FILING DATE: 1998-11-19

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.2

; SEQ ID NO 2

; LENGTH: 1436

; TYPE: DNA

; ORGANISM: Oryza sativa

Query Match 100.0%; Score 1436; DB 9; Length 1436;
Best local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGGAATCATCTCCAGCCTACATGTACTCTCTCCCATATAACAAGTGTCTATGA 60
Db 1 CATTGGAATCATCTCCAGCCTACATGTACTCTCTCCCATATAACAAGTGTCTATGA 60
QY 61 TTCAAAATTTGTCTACAAATATAACATTTCCAGCATGAAATCCATTAATTTTCAG 120
Db 61 TTCAAAATTTGTCTACAAATATAACATTTCCAGCATGAAATCCATTAATTTTCAG 120
QY 121 CTAATCAGATGCTTGAGGGAATAAATCTAAGCGATTCAATATGCAAAAATGATCAGTGA 180
Db 121 CTAATCAGATGCTTGAGGGAATAAATCTAAGCGATTCAATATGCAAAAATGATCAGTGA 180
QY 181 AGTAAGTGAAGAAGATATCTCGTTTAAACATTAGTCTAGTATTTAACAACATGAA 240
Db 181 AGTAAGTGAAGAAGATATCTCGTTTAAACATTAGTCTAGTATTTAACAACATGAA 240
QY 241 AAATGTTTATATTTTAGTACAAATCCAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG 300
Db 241 AAATGTTTATATTTTAGTACAAATCCAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG 300
QY 301 TGTTCGGATCACCCTGAGAAACCGTCAAGGTGTTGTCTGTGCGGTCCAGCCGATCAGAAAT 360
Db 301 TGTTCGGATCACCCTGAGAAACCGTCAAGGTGTTGTCTGTGCGGTCCAGCCGATCAGAAAT 360
QY 361 TCGGAGATCCGCCGTGTTCTTTCTGAAATCTGCAAGTCCAGACGACGACGACGACGACG 420
Db 361 TCGGAGATCCGCCGTGTTCTTTCTGAAATCTGCAAGTCCAGACGACGACGACGACGACG 420
QY 421 AGCAAGACCAATGGCGTGACAGGAGTTGATACCTTGATGACACTAGCTAGCTAGGCG 480
Db 421 AGCAAGACCAATGGCGTGACAGGAGTTGATACCTTGATGACACTAGCTAGCTAGGCG 480
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Db 481 TTGCTTCATGTGCTCTCAGCCGCGCGGAATGTGCCATGATCTGCATGCATCATCGCC 540
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Db 541 AAGATTATATCTCTCACAATTTTCTTCTCTATCGCTCCTAGTGTCTGTTGGAGCTTA 600
QY 601 AAATTATGAAAAAGCAGCTGCTGAGAACTAGCTGTGAGAACTGAAAGAAATTGAGTTCT 660
Db 601 AAATTATGAAAAAGCAGCTGCTGAGAACTAGCTGTGAGAACTGAAAGAAATTGAGTTCT 660
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Db 661 ACGTTCATCTCCAGATTCTACAATTAAGATTCTTATTAATTAGTAAAAAGCTGACT 720
QY 721 GTTGGAGCTTCTGTGACCGGAGATTCTGTGAGAACTGACGCTGCTAGAAGCTTCCC 780
Db 721 GTTGGAGCTTCTGTGACCGGAGATTCTGTGAGAACTGACGCTGCTAGAAGCTTCCC 780
QY 781 CAAACAGACCCCTAGTGTACTCTAGCTGATCGATTCACTCTATTTTATATACACCTTGC 840
Db 781 CAAACAGACCCCTAGTGTACTCTAGCTGATCGATTCACTCTATTTTATATACACCTTGC 840
QY 841 TCTCTAGCTTATCAAAAGTAGCCAGAACTGGAATTTTAAAGCTTAAATGATTTGATGT 900
Db 841 TCTCTAGCTTATCAAAAGTAGCCAGAACTGGAATTTTAAAGCTTAAATGATTTGATGT 900
QY 901 TCTTTTCATCGTAATTCACCTTACCGAAGCTTAGTGGCATTGGAATTTTAAAAATAATTT 960
Db 901 TCTTTTCATCGTAATTCACCTTACCGAAGCTTAGTGGCATTGGAATTTTAAAAATAATTT 960
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Db 1021 CCTATAAATTTATTTATTTTTCAGCGGAGTAGCATTTAGTGTATGGTTATATCATCTGG 1080
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Db 1081 TATGCTTAAATCTCTTACTTGGAGCTTAGTGGAGCAATTGCAATGCAATTCTCGTGCCA 1140
QY 1141 TCTCTATAATACGGCCCTGTAGCTTTGCTCTGTATCTGACACACAAGAACTAGTGGCAA 1200
Db 1141 TCTCTATAATACGGCCCTGTAGCTTTGCTCTGTATCTGACACACAAGAACTAGTGGCAA 1200
QY 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTCTCCAGCTCTCCCATGGCGTCCCTGCT 1260
Db 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTCTCCAGCTCTCCCATGGCGTCCCTGCT 1260
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Db 1261 CGCCATCGCCATCGCCATGGCTCTCATGTGTGACAGAGATATCCAGCATGCTGAAATTAAT 1320
QY 1321 TGACGATATCATCTCATCATCACTTGCAATTTCAACTTCTGATTTGTGACAGACATGTTTA 1380
Db 1321 TGACGATATCATCTCATCATCACTTGCAATTTCAACTTCTGATTTGTGACAGACATGTTTA 1380
QY 1381 GCTGATCAGTAAACGTTGCCGTTGTAATTGTTCTCTTATCAGGTGTTCAACCTGG 1436
Db 1381 GCTGATCAGTAAACGTTGCCGTTGTAATTGTTCTCTTATCAGGTGTTCAACCTGG 1436

RESULT 2
US-10-602-166-2
; Sequence 2, Application US/10602166
; Publication No. US20040060084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHER-SPECIFIC GENE AND TRANSGENIC PLANT TR
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/10/602,166
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 2
; LENGTH: 1436
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-602-166-2

Query Match 100.0%; Score 1436; DB 18; Length 1436;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTGGAATCATCTCCAGCCTACATGTACTCTCTCCCATATAACAAGTGTCTATGA 60
Db 1 CATTGGAATCATCTCCAGCCTACATGTACTCTCTCCCATATAACAAGTGTCTATGA 60
QY 61 TTCAAAATTTGTCTCTACAAATATAACATTTCCAGCATGAAATCCATTAATTTTCAG 120
Db 61 TTCAAAATTTGTCTCTACAAATATAACATTTCCAGCATGAAATCCATTAATTTTCAG 120
QY 121 CTAATCAGATGCTTGAGGGAATAAATCTAAGCGATTCAATATGCAAAAATGATCAGTGA 180
Db 121 CTAATCAGATGCTTGAGGGAATAAATCTAAGCGATTCAATATGCAAAAATGATCAGTGA 180
QY 181 AGTAAGTGAAGAAGATATCTCGTTTAAACATTAGTCTAGTATTTAACAACATGAA 240
Db 181 AGTAAGTGAAGAAGATATCTCGTTTAAACATTAGTCTAGTATTTAACAACATGAA 240
QY 241 AAATGTTTATATTTTAGTACAAATCCAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG 300

Db 241 AAATTGTTATATTTAGTACAAATCGAGTAGTAGAGTAGACAGAGCTAGCGTTAAGATCG 300
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Db 301 TGTTCGATCACCCTGAGAAAACCGTCAGGTGTTGTCTGTGCCGTCAGCCGATCAGAAT 360
QY 361 TCGAGATCCGCGCTCTTCTTCTGAAATCGCAAGTCCAGCAGCAGCAGCAG 420
Db 361 TCGAGATCCGCGCTCTTCTTCTGAAATCGCAAGTCCAGCAGCAGCAGCAGCAG 420
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Db 541 AAGATTATATTCCTCACATTTTCTTCTCTATCGCTCTAGTGTCTGTGGAGCTTA 600
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Db 721 GTTTGGAGCTTCTGTCAAGCCGAGATTCTGTGAGAAAGCTGCAAGCTTCCC 780
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Db 781 CAAACAGACCCCTAGTGTGTACTCTAGCTGATGATTCATCTATTTATATACACCTTGC 840
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Db 841 TCTCTAGCTTATCAAAAGTAGCCAAAGACTTGAATTTTAAAGCTTAAATGATTTGATGT 900
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Db 961 TTAGAGCTGATTTGATTTTTCAGCGGAAATTTATTTTCAAGTATGTAAGAAAGTTT 1020
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QY 1081 TATGCTTAATCTCTTACTTGAAGTATGAGCAATTCGTAATGCAATTCCTGCGCA 1140
Db 1081 TATGCTTAATCTCTTACTTGAAGTATGAGCAATTCGTAATGCAATTCCTGCGCA 1140
QY 1141 TCTCTATAATAGGCGCTGCTAGCTTGTCTGTATCTGCACACAGAACTAGTGCAA 1200
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QY 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTCCAGCTCCTCCATGCGCTCCCTCGT 1260
Db 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTCCAGCTCCTCCATGCGCTCCCTCGT 1260
QY 1261 CGCCATCGCCATCGCCATGCGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTTAACT 1320
Db 1261 CGCCATCGCCATCGCCATGCGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTTAACT 1320
QY 1321 TGAAGCATATCATCTCATCATCACTTGCATTTCAACTTCTGATTTGTGAGACATGTTTA 1380
Db 1321 TGAAGCATATCATCTCATCATCACTTGCATTTCAACTTCTGATTTGTGAGACATGTTTA 1380

Db 1321 TGAAGCATATCATCTCATCATCACTTGCATTTCAACTTCTGATTTGTGAGACATGTTTA 1380
QY 1381 GCTGATCAGTAACGTTGCCGTTGTAATTTGCTCTTATCAGGTGTTCAACCTGG 1436
Db 1381 GCTGATCAGTAACGTTGCCGTTGTAATTTGCTCTTATCAGGTGTTCAACCTGG 1436
RESULT 3
US-09-848-696-1
; Sequence 1, Application US/09848696
; Patent No. US20010051713A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHHER-SPECIFIC GENE AND TRANSGENIC PLANT TR-
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 1
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-848-696-1
Query Match 100.0%; Score 1436; DB 9; Length 3003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CATTCAGAAATCATCTCCAGCCCTAAGTACTCTCTCCCAATAACAAGTCTCTATGA 60
Db 1 CATTCAGAAATCATCTCCAGCCCTAAGTACTCTCTCCCAATAACAAGTCTCTATGA 60
QY 61 TTCAAAATTTGCTCTACATATTAACATTTCCAGCATGAATCCATACATTAATTTTCAG 120
Db 61 TTCAAAATTTGCTCTCTACATATTAACATTTCCAGCATGAATCCATACATTAATTTTCAG 120
QY 121 CTAATCAGATGCTTGAGGGGAAAATCTAAGCGATTCAATATGCAAAAATTGATCACTGA 180
Db 121 CTAATCAGATGCTTGAGGGGAAAATCTAAGCGATTCAATATGCAAAAATTGATCACTGA 180
QY 181 AGTAAGTGAAGAGAAATATCTCGTTTAAACATTAAGTCTAGTATTTAATAACAATAAA 240
Db 181 AGTAAGTGAAGAGAAATATCTCGTTTAAACATTAAGTCTAGTATTTAATAACAATAAA 240
QY 241 AAATGTTTATATTTTAAAGTAAATCGAGTAGTAGCAGTAGCAGTAGCAGTAGCAGTAGC 300
Db 241 AAATGTTTATATTTTAAAGTAAATCGAGTAGTAGCAGTAGCAGTAGCAGTAGCAGTAGC 300
QY 301 TGTTCGATCACTGAGAAACCGTCAAGTGTGTTGTCTGTGCCGTCAGCCGATCAGAAT 360
Db 301 TGTTCGATCACTGAGAAACCGTCAAGTGTGTTGTCTGTGCCGTCAGCCGATCAGAAT 360
QY 361 TCGGAGATCCGCGCTGTTCTTCTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAG 420
Db 361 TCGGAGATCCGCGCTGTTCTTCTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAGCAG 420
QY 421 AGCAAGAGCAATGGCGTGACAGGAGTTGATACCTTTGATGCACTAGCTAGCTAGGCG 480
Db 421 AGCAAGAGCAATGGCGTGACAGGAGTTGATACCTTTGATGCACTAGCTAGCTAGGCG 480
QY 481 TTCGTTCCATGTGCGTCTCAAGCCGTCGAATGTCATGATCCTGCATGATCAGCC 540
Db 481 TTCGTTCCATGTGCGTCTCAAGCCGTCGAATGTCATGATCCTGCATGATCAGCC 540

QY	541	AAGATTATATTCCTCACATTTTCTTCTCTATCGCTCCCTAGTCGTCTGTTGGAGCTTA	600
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QY	601	AAATTATGAAAAGCAGCTGCTGAGAGCTAGCTGCTGAGAACTGGAAGAAATTGAGTCT	660
Db	601	AAATTATGAAAAGCAGCTGCTGAGAGCTAGCTGCTGAGAACTGGAAGAAATTGAGTCT	660
QY	661	ACGTTCAATCTCCAGATTCACAATTAACAGATTCCTATAATTAGTAAAAAGCTGACT	720
Db	661	ACGTTCAATCTCCAGATTCACAATTAACAGATTCCTATAATTAGTAAAAAGCTGACT	720
QY	721	GTTTGGAGCTTCTGTCAAGCCGAGATTCGTGAGAGCTGCAGCTGCTAGAAGCTTCCC	780
Db	721	GTTTGGAGCTTCTGTCAAGCCGAGATTCGTGAGAGCTGCAGCTGCTAGAAGCTTCCC	780
QY	781	CAACACAGACCCCTAGTTGTACTCTAGCTGATCGATTTCACCTTAATTTATATACACCTTGC	840
Db	781	CAACACAGACCCCTAGTTGTACTCTAGCTGATCGATTTCACCTTAATTTATATACACCTTGC	840
QY	841	TCCTAGCTTATCAAACGCTAGCCCAAAGCTTGAATTTTAAAGCTTAAATTGATTTTGATGT	900
Db	841	TCCTAGCTTATCAAACGCTAGCCCAAAGCTTGAATTTTAAAGCTTAAATTGATTTTGATGT	900
QY	901	TCCTTTTCATCGTAATTCACCTTACCGACCTTAGTCGGCATTGGAATTTTAAAAATAATTT	960
Db	901	TCCTTTTCATCGTAATTCACCTTACCGACCTTAGTCGGCATTGGAATTTTAAAAATAATTT	960
QY	961	TTAGAGCTGATTTTGATTTTCTTTCAGCGGAATTTATTTTCAAGTATGTAAAAAGTTTAA	1020
Db	961	TTAGAGCTGATTTTGATTTTCTTTCAGCGGAATTTATTTTCAAGTATGTAAAAAGTTTAA	1020
QY	1021	CCTATAAATTATTAAATTTTTCAGCGGAGTAAGCATTAGTGTATGGTTATAATCATCTGG	1080
Db	1021	CCTATAAATTATTAAATTTTTCAGCGGAGTAAGCATTAGTGTATGGTTATAATCATCTGG	1080
QY	1081	TATGCTTAAATCTCTTACTTGAAGCTTAGTTGGACAATTCGTAATGCATCTCTCGCCA	1140
Db	1081	TATGCTTAAATCTCTTACTTGAAGCTTAGTTGGACAATTCGTAATGCATCTCTCGCCA	1140
QY	1141	TCCTATAATTAAGGCGCTGCTAGCTTCTCTGTATCTGACAACAAGAACTAGCTGGCAA	1200
Db	1141	TCCTATAATTAAGGCGCTGCTAGCTTCTCTGTATCTGACAACAAGAACTAGCTGGCAA	1200
QY	1201	AGTCCTCAAGGCGAACCCTCCATCTTCTCTCTTCCAGCTCTCCCATGGCGTCCCTCGT	1260
Db	1201	AGTCCTCAAGGCGAACCCTCCATCTTCTCTCTTCCAGCTCTCCCATGGCGTCCCTCGT	1260
QY	1261	CGCCATCGCCATCGCCATGGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTAACT	1320
Db	1261	CGCCATCGCCATCGCCATGGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTAACT	1320
QY	1321	TGACGCATATCATCTCATCACTGATTCATTTCAACTTCTGAAATGTGACAGACATGTTTA	1380
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QY	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTGGTCTCTTATCAGGTGTTCAACCTGG	1436
Db	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTGGTCTCTTATCAGGTGTTCAACCTGG	1436

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RESULT 4
US-10-602-166-1
; Sequence 1, Application US/10602166
; Publication No. US20040060084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHER-SPECIFIC GENE AND TRANSGENIC PLANT THEREWITH
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A

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: CURRENT APPLICATION NUMBER: US/10/602,166
: CURRENT FILING DATE: 2003-06-24
: PRIOR APPLICATION NUMBER: US/09/848,696
: PRIOR FILING DATE: 2001-05-03
: PRIOR APPLICATION NUMBER: KR 98-46973
: PRIOR FILING DATE: 1998-11-03
: PRIOR APPLICATION NUMBER: KR 98-50126
: PRIOR FILING DATE: 1998-11-19
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: PatentIn Ver. 2.2
: SEQ ID NO 1
: LENGTH: 3003
: TYPE: DNA
: ORGANISM: Oryza sativa
US-10-602-166-1

Query Match      100.0%; Score 1436; DB 18; Length 3003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	241	AAATGTTTATATTTTAGTACAAATCGAGTAGACAGTAGACAGCTAGCGTAAGATCG	300
Db	241	AAATGTTTATATTTTAGTACAAATCGAGTAGACAGTAGACAGCTAGCGTAAGATCG	300
QY	301	TGTTCCGATCACCTGAGAAACCGTCAGGTGTTGTCTGTGCCCTCCAGCCGATCAGAAT	360
Db	301	TGTTCCGATCACCTGAGAAACCGTCAGGTGTTGTCTGTGCCCTCCAGCCGATCAGAAT	360
QY	361	TCCGAGATCCGCCGTCGTTCTTTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAG	420
Db	361	TCCGAGATCCGCCGTCGTTCTTTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAG	420
QY	421	AGCAAGAGCAATGGCGGTGCAAGGAGTTGATACTTTGATGCACTAGCTACTAGGCG	480
Db	421	AGCAAGAGCAATGGCGGTGCAAGGAGTTGATACTTTGATGCACTAGCTACTAGGCG	480
QY	481	TTGTTCCATGTGCTCTCAGCGCGTGCGAATGTGCCATGATCTGCATCATCGCC	540
Db	481	TTGTTCCATGTGCTCTCAGCGCGTGCGAATGTGCCATGATCTGCATCATCGCC	540
QY	541	AAGATTATATTCCTCACATTTTCTTCTCTATCGCTCCTAGTCGTGTTGGAGCTTA	600
Db	541	AAGATTATATTCCTCACATTTTCTTCTCTATCGCTCCTAGTCGTGTTGGAGCTTA	600
QY	601	AAATATGAAAAAGCAGCTGCTGAGAAGCTAGCTGAGAAATCGAAGAAATTTGAGTCT	660
Db	601	AAATATGAAAAAGCAGCTGCTGAGAAGCTAGCTGAGAAATCGAAGAAATTTGAGTCT	660
QY	661	ACGTTCAATCTCCAGATTCTACAATTAACAGATTCTTAATTAAGTAAAAAGCTGACT	720
Db	661	ACGTTCAATCTCCAGATTCTACAATTAACAGATTCTTAATTAAGTAAAAAGCTGACT	720
QY	721	GTTTGGAGCTTCTGTCAAGCGGAGATTCTGTGAGAGCTGCACTGCTAGAAGCTTCCC	780
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QY	781	CAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCACTCTATTATATACACCTTGC	840

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QY 841 TCTTAGCTTATCAAAAGTAGCCCAAGACTTGAAATTTTAAAGCTTAAATTGATTTGATGT 900
Db 841 TCTTAGCTTATCAAAAGTAGCCCAAGACTTGAAATTTTAAAGCTTAAATTGATTTGATGT 900
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Db 901 TCTTTTCATCGTAATCACTTACCGACCTTAGTCGCATTTGAATTTTAAATAATTTT 960
QY 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTATTTTCACGTATGTAAAGTTT 1020
Db 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTATTTTCACGTATGTAAAGTTT 1020
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QY 1141 TCTCTATAATACGGCTGTAGCTTGTCTCTGTATCTGCACACAAAGAACTAGCTGGCAA 1200
Db 1141 TCTCTATAATACGGCTGTAGCTTGTCTCTGTATCTGCACACAAAGAACTAGCTGGCAA 1200
QY 1201 AGTCCTCAAGGCGAACCGCTCCATCTTCTCTCCAGCTCCCTCCAGGCGTCCCTCGT 1260
Db 1201 AGTCCTCAAGGCGAACCGCTCCATCTTCTCTCCAGCTCCCTCCAGGCGTCCCTCGT 1260
QY 1261 CGCCATCGCCATCGCCATGGCTCTCATGTGTGACAGATATCCAGCATGCTGAATTAAT 1320
Db 1261 CGCCATCGCCATCGCCATGGCTCTCATGTGTGACAGATATCCAGCATGCTGAATTAAT 1320
QY 1321 TGACGCATATCATCTCATCATCACTTGCAATTTCAACTTGTGACAGATGTT 1380
Db 1321 TGACGCATATCATCTCATCATCACTTGCAATTTCAACTTGTGACAGATGTT 1380
QY 1381 GCTGATCAGTAAACGTTGCCGTGTGAATGGTCTTATCAGGTGTGTTCAACTGG 1436
Db 1381 GCTGATCAGTAAACGTTGCCGTGTGAATGGTCTTATCAGGTGTGTTCAACTGG 1436

RESULT 5

US-09-848-696-3
; Sequence 3, Application US/09848696
; Patent No. US20010051713A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHR- SPECIFIC GENE AND TRANSGENIC PLANT TRA
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/09/848,696
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatencIn Ver. 2.2
; SEQ ID NO 3
; LENGTH: 1196
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-848-696-3

Query Match 83.3%; Score 1196; DB 9; Length 1196;
Best Local Similarity 100.0%; Pred. No. 5e-281;
Matches 1196; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGAGATCATCTCCAGCCCTACAAATGTACTCTCTCCCAATAACAAAGTGTCTATAGA 60
Db 1 CATTGAGATCATCTCCAGCCCTACAAATGTACTCTCTCCCAATAACAAAGTGTCTATAGA 60
QY 61 TTCAAAATTTGCTCTACAAATTAACAATTTCCAGCATGAATCCATTAATTTTCAG 120
Db 61 TTCAAAATTTGCTCTACAAATTAACAATTTCCAGCATGAATCCATTAATTTTCAG 120
QY 121 CTATCAGATGCTTGAGGGAATAATCTAAGCATTCATATGCAAAAATGATCACTGA 180
Db 121 CTATCAGATGCTTGAGGGAATAATCTAAGCATTCATATGCAAAAATGATCACTGA 180
QY 181 AGTAACGAAAGAGATATCTCGTTTAAACATTAAGTGTATTTAATTAACAATAA 240
Db 181 AGTAACGAAAGAGATATCTCGTTTAAACATTAAGTGTATTTAATTAACAATAA 240
QY 241 AAATTGTTATATTTTATAGTACAAATCGAGTAGTAGCAGTAGCAGCTAGCGTAAGATCG 300
Db 241 AAATTGTTATATTTTATAGTACAAATCGAGTAGTAGCAGTAGCAGCTAGCGTAAGATCG 300
QY 301 TGTTCCGATCACTGAGAAACCGTCAGGTGTTGTCTGTGCGCTCCAGCCGATCAGAAAT 360
Db 301 TGTTCCGATCACTGAGAAACCGTCAGGTGTTGTCTGTGCGCTCCAGCCGATCAGAAAT 360
QY 361 TCGGAGATCCCGCTGCTTCTTCTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAG 420
Db 361 TCGGAGATCCCGCTGCTTCTTCTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAG 420
QY 421 AGCAAGAGCAATGGCGTGCAGGAGTTGTATACCTTTGATGCACTAGCTACTAGGCG 480
Db 421 AGCAAGAGCAATGGCGTGCAGGAGTTGTATACCTTTGATGCACTAGCTACTAGGCG 480
QY 481 TTGCTTCATGTGCTCTCACGCCGTGCGAATGTGCCATGATCTGCATGCATCGCC 540
Db 481 TTGCTTCATGTGCTCTCACGCCGTGCGAATGTGCCATGATCTGCATGCATCGCC 540
QY 541 AAGATTAATTCCTCACATTTTCTTCTATCGCTCTAGTGTCTGTTGGAGCTTA 600
Db 541 AAGATTAATTCCTCACATTTTCTTCTATCGCTCTAGTGTCTGTTGGAGCTTA 600
QY 601 AAATTGAAGAAAGCAGCTGCTGAGAGCTAGCTGTGAGAAATCGAAGATTTGATTTCT 660
Db 601 AAATTGAAGAAAGCAGCTGCTGAGAGCTAGCTGTGAGAAATCGAAGATTTGATTTCT 660
QY 661 ACGTTCAATCTCCAGATTCTTACAATTAACAGATTCTTATTAATTAAGTAAAGCTGACT 720
Db 661 ACGTTCAATCTCCAGATTCTTACAATTAACAGATTCTTATTAATTAAGTAAAGCTGACT 720
QY 721 GTTTGGAGCTTCTGTACGCCGAGATTCTGTGAGAGCTGAGCTGTAGAGCTTCCC 780
Db 721 GTTTGGAGCTTCTGTACGCCGAGATTCTGTGAGAGCTGAGCTGTAGAGCTTCCC 780
QY 781 CAAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCATCTATTTATATACACCTTGC 840
Db 781 CAAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCATCTATTTATATACACCTTGC 840
QY 841 TCTTAGCTTATCAAAAGTAGCCCAAGACTTGAAATTTTAAAGCTTAAATTGATTTGATGT 900
Db 841 TCTTAGCTTATCAAAAGTAGCCCAAGACTTGAAATTTTAAAGCTTAAATTGATTTGATGT 900
QY 901 TCTTTTCATCGTAATCACTTACCGACCTTAGTCGCATTTGAATTTTAAATAATTTT 960
Db 901 TCTTTTCATCGTAATCACTTACCGACCTTAGTCGCATTTGAATTTTAAATAATTTT 960
QY 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTATTTTCACGTATGTAAAGTTT 1020
Db 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTATTTTCACGTATGTAAAGTTT 1020
QY 1021 CCTATAATTAATTAATTTTCAGCGGAGTAAGCAATTAGTGTATGGGTAAATCATCTGG 1080
Db 1021 CCTATAATTAATTAATTTTCAGCGGAGTAAGCAATTAGTGTATGGGTAAATCATCTGG 1080

[illegible]

RESULT 6

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US-10-602-166-3
/ Sequence 3, Application US/10602166
/ Publication No. US20040060084A1
/ GENERAL INFORMATION:
/ APPLICANT: AN, GYN HEUNG
/ APPLICANT: JEON, JONG-SEONG
/ APPLICANT: CHUNG, YONG-YOON
/ APPLICANT: LEE, SI CHUL
/ TITLE OF INVENTION: DNA COMPRISING RICE ANTHR- SPECIFIC GENE AND TRANSGENIC PLANT TRA
/ TITLE OF INVENTION: THEREWITH
/ FILE REFERENCE: S-30723A
/ CURRENT APPLICATION NUMBER: US/10/602,166
/ CURRENT FILING DATE: 2003-06-24
/ PRIOR APPLICATION NUMBER: US/09/848,696
/ PRIOR FILING DATE: 2001-05-03
/ PRIOR APPLICATION NUMBER: KR 98-46973
/ PRIOR FILING DATE: 1998-11-03
/ PRIOR APPLICATION NUMBER: KR 98-50126
/ PRIOR FILING DATE: 1998-11-19
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.2
/ SEQ ID NO 3
/ LENGTH: 1196
/ TYPE: DNA
/ ORGANISM: Oryza sativa
US-10-602-166-3

```

Query Match	83.3%	Score 1196;	DB 18;	Length 1196;
Best Local Similarity	100.0%;	Pred. No. 5e-281;		
Matches 1196;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

OY		1	CATTGAGATCATCTCCAGCCTACAATGTACTCTCCCATATACAAGTGTCTATGA	60
Dp		1	CATTGAGAATCATCTCCAGCCTACAATGTACTCTCCCATATACAAGTGTCTATGA	60
OY		61	TTCAAAATTTGTCCTACATATAAACATTTCCAGCATGAAATCCATACATTAA	120
Dp		61	TTCAAAATTTGTCCTACATATAAACATTTCCAGCATGAAATCCATACATTAA	120
OY		121	CTAATCAGATGCTTGAGGGAAAAATCTAAGCATTCATATGC AAAATTGATCACTGA	180
Dp		121	CTAATCAGATGCTTGAGGGAAAAATCTAAGCATTCATATGC AAAATTGATCACTGA	180
OY		181	AGTAAC TGAAGA GAAATATCTCGTTTAACTTAGTGTAGTATTATTAACA CTAAA	240
Dp		181	AGTAAC TGAAGA GAAATATCTCGTTTAACTTAGTGTAGTATTATTAACA CTAAA	240
OY		241	AAATGTTTATATTTTAGTACA AATCGAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300
Dp		241	AAATGTTTATATTTTAGTACA AATCGAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300
OY		301	TGTTCCGATCACCTGAGAAACC GTCAGGTGTTGTCTGTGCCGTCCAGCCGATCAGAAT	360
Dp		301	TGTTCCGATCACCTGAGAAACC GTCAGGTGTTGTCTGTGCCGTCCAGCCGATCAGAAT	360
OY		361	TCCGAGATCCGCCGTGTTCTTTCTGAAA TCTGCAAGTCCAGCAGCAGCAGCAG	420
Dp		361	TCCGAGATCCGCCGTGTTCTTTCTGAAA TCTGCAAGTCCAGCAGCAGCAGCAGCAG	420
OY		421	AGCAGAGCAATGCGCTG CAGGAGTTTGATCTTGATGC ACTAGCTAGCTAGGCG	480
Dp		421	AGCAGAGCAATGCGCTG CAGGAGTTTGATCTTGATGC ACTAGCTAGCTAGGCG	480
OY		481	AGCAGAGCAATGCGCTG CAGGAGTTTGATCTTGATGC ACTAGCTAGCTAGGCG	540
Dp		481	AGCAGAGCAATGCGCTG CAGGAGTTTGATCTTGATGC ACTAGCTAGCTAGGCG	540

Qy	481	TTGCTTCATGTCGCTCTCAGCCGCTGCGAATGTCATGATCCCTGCATGCATCATCGCC	540
	481	TTGCTTCATGTCGCTCTCAGCCGCTGCGAATGTCATGATCCCTGCATGCATCATCGCC	540
Qy	541	AAGATTATATTTCTTCACATTTTTTTCTTCCATCGCTCCTAGTCGTCGTGGGAGCTTA	600
	541	AAGATTATATTTCTTCACATTTTTTTCTTCCATCGCTCCTAGTCGTCGTGGGAGCTTA	600
Qy	601	AAATTATGAAAGACAGCTGCTGAGAAGCTAGCTGCTGAGAATCTGAAGAAATTTGAGTCT	660
	601	AAATTATGAAAGACAGCTGCTGAGAAGCTAGCTGCTGAGAATCTGAAGAAATTTGAGTCT	660
Qy	661	ACGTTCAATCTCCAGATTCTACAATTACAGATTCTTATTAATTTAGGTAAAAAGCTGGACT	720
	661	ACGTTCAATCTCCAGATTCTACAATTACAGATTCTTATTAATTTAGGTAAAAAGCTGGACT	720
Qy	721	GTTTGGAGCTTCTGTCAAGCCGGAGATTCTGTGAGAAAGCTGCAGCTGCTAGAGCTTCCC	780
	721	GTTTGGAGCTTCTGTCAAGCCGGAGATTCTGTGAGAAAGCTGCAGCTGCTAGAGCTTCCC	780
Qy	781	CAACACAGACCCCTAGTTGTACTCTAGCTGATCGAATTCACCTATTTTATATACACCTTGC	840
	781	CAACACAGACCCCTAGTTGTACTCTAGCTGATCGAATTCACCTATTTTATATACACCTTGC	840
Qy	841	TCTCTAGCTTATCAAACGTAGCCAGAAGCTTGAATTTTAAAGCTTAAATTGATTTTGATGT	900
	841	TCTCTAGCTTATCAAACGTAGCCAGAAGCTTGAATTTTAAAGCTTAAATTGATTTTGATGT	900
Qy	901	TCTTTTCATCGTAATTCACCTTACCGACCTTAGTCGGCAATTTGAATTTTAAAAATAATTT	960
	901	TCTTTTCATCGTAATTCACCTTACCGACCTTAGTCGGCAATTTGAATTTTAAAAATAATTT	960
Qy	961	TTAGAGCTGATTTTGAATTTTTTTTTCAGCGGAATTTATTTTACCGTATGTAAAGTTTAA	1020
	961	TTAGAGCTGATTTTGAATTTTTTTTTCAGCGGAATTTATTTTACCGTATGTAAAGTTTAA	1020
Qy	1021	CCTATAAATTATTAATTTTCAGCGGAGTAAGCAATTAAGTTATGAGTTATTAATCATCTGG	1080
	1021	CCTATAAATTATTAATTTTCAGCGGAGTAAGCAATTAAGTTATGAGTTATTAATCATCTGG	1080
Qy	1081	TATGCTTAATCTCTTTACTTGGACTTAGTTGGACAATTCGTAATGCATTTCTCGTGCCA	1140
	1081	TATGCTTAATCTCTTTACTTGGACTTAGTTGGACAATTCGTAATGCATTTCTCGTGCCA	1140
Qy	1141	TCTCTATAATACGGCTGCTAGCTTTGCTCTTGTATCTGCACACAAAGAACTAGCTG	1196
	1141	TCTCTATAATACGGCTGCTAGCTTTGCTCTTGTATCTGCACACAAAGAACTAGCTG	1196

RESULT 7

```

US-09-848-696-10
; Sequence 10, Application US/09848696
; Patent No. US20010051713a1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHR-SPCIFIC GENE AND TRANSGENIC PLANT TRA
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/09/848,696
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.2
; SEQ ID NO 10
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Oryza sativa

```

US-09-848-696-10

Query Match 16.7%; Score 240; DB 9; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.4e-48;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCAAGCGCAACCGCTCCATCTTCTCTCCAGCTCCTCCCATGGCGTCCC 1256
DB 1 GCAAGTCTCAAGCGCAACCGCTCCATCTTCTCTCCAGCTCCTCCCATGGCGTCCC 60
QY 1257 TCGTCGCATCGCCATCGCCATGGCTCTCATGTCAGAGATATCCAGCATGCTGAATT 1316
DB 61 TCGTCGCATCGCCATCGCCATGGCTCTCATGTCAGAGATATCCAGCATGCTGAATT 120
QY 1317 AACTGACGATATCATCTCATCATCACTTGCACTTCACTTGTGATTGTCAGACATG 1376
DB 121 AACTGACGATATCATCTCATCATCACTTGCACTTCACTTGTGATTGTCAGACATG 180
QY 1377 TTAGCTGATCAGTAAACGTTGCCGTGTGAATTGCTCTTATCAGGTGTTCAACCTGG 1436
DB 181 TTAGCTGATCAGTAAACGTTGCCGTGTGAATTGCTCTTATCAGGTGTTCAACCTGG 240

RESULT 8

US-10-602-166-10
; Sequence 10, Application US/10602166
; Publication No. US2004006084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHR-SPESIFIC GENE AND TRANSGENIC PLANT TRA
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/10/602,166
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.2
; SEQ ID NO 10
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-602-166-10

Query Match 16.7%; Score 240; DB 18; Length 240;
Best Local Similarity 100.0%; Pred. No. 3.4e-48;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCAAGCGCAACCGCTCCATCTTCTCTCCAGCTCCTCCCATGGCGTCCC 1256
DB 1 GCAAGTCTCAAGCGCAACCGCTCCATCTTCTCTCCAGCTCCTCCCATGGCGTCCC 60
QY 1257 TCGTCGCATCGCCATCGCCATGGCTCTCATGTCAGAGATATCCAGCATGCTGAATT 1316
DB 61 TCGTCGCATCGCCATCGCCATGGCTCTCATGTCAGAGATATCCAGCATGCTGAATT 120
QY 1317 AACTGACGATATCATCTCATCATCACTTGCACTTCACTTGTGATTGTCAGACATG 1376
DB 121 AACTGACGATATCATCTCATCATCACTTGCACTTCACTTGTGATTGTCAGACATG 180
QY 1377 TTAGCTGATCAGTAAACGTTGCCGTGTGAATTGCTCTTATCAGGTGTTCAACCTGG 1436
DB 181 TTAGCTGATCAGTAAACGTTGCCGTGTGAATTGCTCTTATCAGGTGTTCAACCTGG 240

RESULT 9

US-10-437-963-87679

; Sequence 87679, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 87679
; LENGTH: 712
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86601C.1
US-10-437-963-87679

Query Match 7.5%; Score 107.4; DB 19; Length 712;
Best Local Similarity 71.4%; Pred. No. 1.3e-15;
Matches 175; Conservative 0; Mismatches 56; Indels 14; Gaps 2;

QY 585 TCTGTTGGAGCTTAAATTTGAAAGCAGCTGCTGAGAGCTAGCTGTGAGAAATCT 644
DB 98 TGTTGGGGAGCTTAAGATTCTGAGAGCAGCTGCTGAGAGCTAGCTGTGAAATTT 157
QY 645 GAAGATTGAGTTCTAC-----GTTCAATCTCCAGATTCTACAATTACAGAT 692
DB 158 GGAGAGCTGGAAGAACCCAGCTTCTAGCTTGTTCATTCTTACATTCTACACTACAGAT 217
QY 693 TCTTAAATTTAGTAAAGCTGACCTGTT--GGAGCTTCTGTCAGCCGAGATTCT 750
DB 218 TCTTAAATTTAGTAAAGCTGAAATTTGTTGAGGAGCTTCTGTAAGCTGAGATTCT 277
QY 751 GTGAGAGCTGACGCTGCTAGAGCTTCCCAAGACAGCCCTAGTTGTAAGCTGAGTGA 810
DB 278 ATAGAGAGATGTAAGCTGCTAGAGCTCCCTAAGACAGCCCTTATGATGACTTAAACATGA 337
QY 811 TCGAT 815
DB 338 TCGTT 342

RESULT 10

US-09-848-696-7
; Sequence 7, Application US/09848696
; Patent No. US20010051713A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHR-SPESIFIC GENE AND TRANSGENIC PLANT TRA
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/09/848,696
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentln Ver. 2.2
; SEQ ID NO 7
; LENGTH: 1008


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; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-848-696-7

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 1256
Db 1 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 60

QY 1257 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 1291
Db 61 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 95

RESULT 11
US-10-602-166-7
; Sequence 7, Application US/10602166
; Publication No. US20040060084A1
; GENERAL INFORMATION:
; APPLICANT: AN, GYN HEUNG
; APPLICANT: JEON, JONG-SEONG
; APPLICANT: CHUNG, YONG-YOON
; APPLICANT: LEE, SI CHUL
; TITLE OF INVENTION: DNA COMPRISING RICE ANTHER-SPECIFIC GENE AND TRANSGENIC PLANT TRA
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: S-30723A
; CURRENT APPLICATION NUMBER: US/10/602,166
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/848,696
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: KR 98-46973
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: KR 98-50126
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.2
; SEQ ID NO 7
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-602-166-7

Query Match
Best Local Similarity 100.0%; Pred. No. 1.7e-12;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 1256
Db 1 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 60

QY 1257 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 1291
Db 61 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 95

RESULT 12
US-10-425-114-30221
; Sequence 30221, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven B
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 30221
; LENGTH: 1054
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-OSROM202018E07_FLI
US-10-425-114-30221

Query Match
Best Local Similarity 98.9%; Pred. No. 4.3e-12;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 1256
Db 1 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 60

QY 1257 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 1291
Db 61 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 95

RESULT 13
US-10-437-963-72585
; Sequence 72585, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 72585
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1250)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72950C.1
US-10-437-963-72585

Query Match
Best Local Similarity 98.9%; Pred. No. 4.7e-12;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1197 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 1256
Db 13 GCAAGTCTCTCAAGCGGAACCGCTCCATCTTCTCTCCAGCTCTCCCATGGCGTCCC 72

QY 1257 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 1291
Db 73 TCGTGGCCATCGCCATCGCCATGGCTCTCATGGTG 107

RESULT 14
US-10-260-238-2616
; Sequence 2616, Application US/10260238
; Publication No. US20040016025A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, Paul R.
```



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; APPLICANT: Moughamer, Todd G.
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
; FILE REFERENCE: 60111-NP
; CURRENT APPLICATION NUMBER: US/10/260,238
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/325,448
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 6077
; SEQ ID NO 2616
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: N_region
; LOCATION: (1496)..(1496)
; OTHER INFORMATION: n = any nucleotide
US-10-260-238-2616

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Matches 155; Conservative 0; Mismatches 46; Indels 17; Gaps 2;
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QY      698 TAATTTAGSTAAAAAGCTGCACTGTTTG--GAGCTTCTGCAGCCGAGATCTGTGAG 755
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; Sequence 4, Application US/10415058
; Publication No. US20040060081A1
; GENERAL INFORMATION:
; APPLICANT: Wisconsin Alumni Research Foundation
; APPLICANT: United States Department Of Agriculture
; APPLICANT: Leong, Sally A.
; APPLICANT: Farnam, Mark L.
; APPLICANT: Chauhan, Rajinder
; APPLICANT: Durfee, Timothy J.
; TITLE OF INVENTION: Plant Gene That Confers Resistance To Strains Of Magnaporthe Gris
; FILE REFERENCE: Warf-0145
; CURRENT APPLICATION NUMBER: US/10/415,058
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: USSN 60/242,313
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: USSN 60/303,897
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 14
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 17953
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-415-058-4
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Best Local Similarity 68.3%; Pred. No. 1.8e-07;
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QY      649 AATTGAGTTCTACGTTCAATTCACAGATTCTACAATTACAGATTCTTAATTAGGTA 708
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Db      17148 AAGTTGGGTT----TTCAACTTCTGGCTTCTATTACTACAGATTCTTAGAACCTGAGTG 17203

QY      709 AAAAGCTGAGCTGTTTGGGAGCTTCTGTCAGCCGAGATTCTGTGAGAACTGCAGCTGC 768
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Db      17204 AGAATGTAGCTAATTGAGG-----AGCTGGAATTCTTAAAGAAACTGCANAATAC 17254

QY      769 TAGAAGCTTCCCAACAGACCCCTAGT 796
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Search completed: September 23, 2005, 19:36:05
Job time : 720 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 23, 2005, 16:39:48 ; Search time 197 Seconds
(without alignments)
11927.377 Million cell updates/sec

Title: US-10-602-166-2
Perfect score: 1436
Sequence: 1 cattcagaatcatctccagc.....taccagtggtccaactgg 1436

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

Database : Issued Patents NA: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	46.2	3.2	7218	1	US-08-232-463-14 Sequence 14, Appl
2	44.8	3.1	13158	2	US-08-687-080-105 Sequence 105, App
3	44.6	3.1	832	4	US-09-621-976-2813 Sequence 2813, Ap
4	43.6	3.0	1664976	4	US-08-916-421B-1 Sequence 1, Appli
5	43.6	3.0	1664976	4	US-09-692-570-1 Sequence 1280, Ap
6	43.4	3.0	1039	4	US-09-902-540-1280 Sequence 1357, Ap
7	42.4	3.0	612	4	US-09-902-540-1357 Sequence 563, App
8	42.4	3.0	740	3	US-08-998-416-563 Sequence 1972, Ap
9	41.8	2.9	570	4	US-09-621-976-1972 Sequence 1448, Ap
10	41.8	2.9	2748	4	US-09-949-016-1448 Sequence 13190, A
11	41.8	2.9	36154	4	US-09-949-016-13190 Sequence 202462,
12	40.6	2.8	601	4	US-09-949-016-202462 Sequence 1, Appli
13	40.4	2.8	6243	2	US-09-056-075-1 Sequence 16065, A
14	40.4	2.8	212139	4	US-09-949-016-16065 Sequence 87645, A
15	40	2.8	601	4	US-09-949-016-87645 Sequence 13, Appl
16	40	2.8	19124	2	US-08-487-826B-13 Sequence 12505, A
17	40	2.8	670689	4	US-09-949-016-12505 Sequence 14207, A
18	40	2.8	670690	4	US-09-949-016-14207 Sequence 3490, Ap
19	39.8	2.8	897	4	US-09-270-767-3490 Sequence 18772, A
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23	39.6	2.8	36618	4	US-09-949-016-16935 Sequence 12550, A
24	39.6	2.8	45842	4	US-09-949-016-12550 Sequence 17327, A
25	39.6	2.8	45842	4	US-09-949-016-17327 Sequence 15189, A
26	39.6	2.8	74730	4	US-09-949-016-15189 Sequence 91213, A
27	39.4	2.7	601	4	US-09-949-016-91213

28	39.4	2.7	601	4	US-09-949-016-91214	Sequence 91214, A
29	39.4	2.7	601	4	US-09-949-016-166398	Sequence 166398,
30	39.4	2.7	164061	4	US-09-949-016-17422	Sequence 17422, A
31	39.4	2.7	167708	4	US-09-949-016-16423	Sequence 16423, A
32	39.4	2.7	175236	4	US-09-949-016-14353	Sequence 14353, A
33	39.4	2.7	636591	4	US-09-949-016-11808	Sequence 11808, A
34	39.4	2.7	636591	4	US-09-949-016-13388	Sequence 13388, A
35	39.2	2.7	601	4	US-09-949-016-122355	Sequence 122355,
36	39.2	2.7	3095	6	5231168-1	Patent No. 5231168
37	39.2	2.7	3095	6	5231168-1	Patent No. 5231168
38	39.2	2.7	133719	4	US-09-949-016-15092	Sequence 15092, A
39	39	2.7	601	4	US-09-949-016-202463	Sequence 202463,
40	39	2.7	2317	3	US-08-749-522-5	Sequence 5, Appli
41	39	2.7	3974	3	US-08-467-504-3	Sequence 3, Appli
42	38.8	2.7	76810	4	US-09-949-016-12528	Sequence 12528, A
43	38.8	2.7	263693	4	US-09-949-016-12386	Sequence 12386, A
44	38.8	2.7	263694	4	US-09-949-016-16915	Sequence 16915, A
45	38.8	2.7	640681	4	US-09-790-988-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; CLONE: PTZgpt-Fls
; US-08-232-463-14
Query Match 3.2%; Score 46.2; DB 1; Length 7218;


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QY      1193 GCTGGCAAGT 1203
Db      343 KYAWARAAARW 353

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; Sequence 1, Application US/08916421B
; Patent No. 6503729
; GENERAL INFORMATION:
; APPLICANT: Buit et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; Patent No. 6503729
; TITLE OF INVENTION: jannaschii
; FILE REFERENCE: PB275
; CURRENT APPLICATION NUMBER: US/08/916,421B
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
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US-08-916-421B-1

Query Match 3.0%; Score 43.6; DB 4; Length 1664976;
Best Local Similarity 47.2%; Pred. No. 4;
Matches 202; Conservative 0; Mismatches 219; Indels 7; Gaps 2;

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US-09-692-570-1
; Sequence 1, Application US/09692570
; Patent No. 6797466
; GENERAL INFORMATION:
; APPLICANT: Bult et al.
; TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanoco
; Patent No. 6797466
; TITLE OF INVENTION: jannaschi
; FILE REFERENCE: PB275C1
; CURRENT APPLICATION NUMBER: US/09/692,570
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US 60/024,428
; PRIOR FILING DATE: 1996-08-22
; PRIOR APPLICATION NUMBER: US 08/916,421
; NUMBER OF SEQ ID NOS: 20
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FEATURE:
NAME/KEY: misc feature
LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a, t, c, or g
```

```
FEATURE:
NAME/KEY: misc feature
LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (713652)..(713652)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1084830)..(1084830)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1313224)..(1313224)
OTHER INFORMATION: n equals a, t, c, or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a, t, c, or g
```

Query Match 3.0%; Score 43.6; DB 4; Length 1664976;

Best Local Similarity 47.2%; Pred. No. 4;

Matches 202; Conservative 0; Mismatches 219; Indels 7; Gaps 2;

```
OY 674 AGATTCTACATTACAGATTCTTATATTAGTTAAAGCTGACTGTTGGAGCTTC 733
Db 251603 AGATTAGCCAAATGAAAAAACCTGAACCTTAAGTTAAAAAGTTATTAGCAAGATAT 251662
```

QY	734	TGTCAGCCGGAGATTCTGTGAGAACTGCAGCTGCTAGAAAGCTTCCCCAAACAGACCCCT	793
Db	251663	GCTAAGCTTTGTAAGTTCAAGCTGATGAGGAGAGCTGTAATTAAAGATATGATTAATAGAGATTT	251722
QY	794	AGTTGTACTCTAGCTGATCGATTCACCTCTATTATTAATACACCTTGCTCTAGCTTAAC	853
Db	251723	CTTAAGCTTAATTGTATTATTTTACATATATTATTTATTAACCAATTAT--AATTTGTC	251779
QY	854	AAACGTAGCCCAAGACTTGAATTTTAAAGCTTAAATGATTTTGATGTTCTTTTCATCGTA	913
Db	251780	GTAATACACTAGGACTAGATTTTAAATTTATATGATTTGGAAAGTTTATCTCGTTCA	251839
QY	914	ATTCACTTACCGACCTTAGTCGGCATTTTGAATTTTAAATAATTTTATAGAGCTGATTT	973
Db	251840	ATACATTTATTAATTAAGAAAAAACCATTTAAATCTGATATCATTAATTTTAAACCTTTT	251899
QY	974	TGATTTTTTTTTTCAGCGGAATTTATTTTCACG---TATGTAAAGTTTACCTATAAAT	1029
Db	251900	TATCTAATTTCTAAGGTAAGCTATTTTAAAAATTTATTTATTTGATTTGTTAAATTA	251959
QY	1030	TATTAAATTTTCAGCGGAGTAAGCATTAAGTGTATGGCTTATTAATCATCTGGTATGCTTAA	1089
Db	251960	TAGGAGATTTTAAAAAATTTCTACTTAATTTGTTTTATTTTGAAGATTTCTCCATGATTAA	252019
QY	1090	ATCTCTTT 1097	
Db	252020	TTTTTATT 252027	

```

RESULT 6
US-09-902-540-1280/c
; Sequence 1280, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1280
; LENGTH: 1039
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(1039)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1280

```

Query Match	3.0%	Score 43.4;	DB 4;	Length 1039;
Best Local Similarity	45.5%;	Pred. No. 0.068;		
Matches 155; Conservative	0;	Mismatches 186;	Indels 0;	Gaps 0;

```
OY      796 TTGTACTCTAGCTGATCGATTCACTCTA TTTTATAATACACCCTTGCTCTAGACTTAACA   855
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     375 TTGTTTTTTTTGTATTTATTTAAATTTTT TTTTATTATTGATGATTTAAATTTTTTTT    316

OY      856 ACGTAGCCAAGACTGAATTTTAAAGCTTAA ATGATTTGGATGTCCTTTTCATCGTAAT   915
       |          | | | | | | | | | | | | | | | | | | | | | | | | |
Db     315 TTTTATATTTTTTTTTTGGATTTTATTATTT ATTATTTTTTTTTTTTTTTTATGTAAT   256

OY      916 TCACCTTACCGACCTTAGTCGCATTTGAAT TTTTAAAAATAATTTTAGAGCTGATTTTG   975
       | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     255 TGTTTTTTTATATATTTTTTTTTTTTTTTT TTTTATAATGTTTTTTTTTTTTTTTTTT    196

OY      976 ATTTTTTTTTCAGCGAATTTA TTTTCCACGTATGTAAAAGTTTACCTATAATTATTA   1035
       ||||||| | | | | | | | | | | | | | | | | | | | | |
```

[illegible]

```

RESULT 7
US-09-902-540-1357/c
; Sequence 1357, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1357
; LENGTH: 612
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(612)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1357

```

Query Match	3.0%	Score 42.4;	DB 4;	Length 612;
Best Local Similarity	48.3%	Pred. No. 0.097;		
Matches 115; Conservative	0;	Mismatches 123;	Indels 0;	Gaps 0;

QY	874	TTTTAAAGCTTAATAATGATTGTGATGTTCTTTTCACATCGTAATTCACCTACCGACCCTTACT	933
Db	437	TTTATATTTTATATTTTATTTT	378
QY	934	CGCATTTGAATTTTAAAAAATATTTTGTAGAGCTGAATTTTGATTTTTTTTTTCAGCGGA	993
Db	377	TTTTTTTATTTTTTTTTTATTTATTTTTTTTTTTTANTTTTTTTTTTTTTTTAT	318
QY	994	TTTATTTTCACGTAATGTAAGAATTTTACCTATAATTTAATTTTCAGCGGAGTAAGCA	1053
Db	317	TTTANTTTTTTTTTTTTAAATTTTTTTTAAATATTTTAAATTTTTTATTTTATTTTATTT	258
QY	1054	TTAGCTTATGGCTATAATCATCTGGTATGCTTAAAATCTCTTTACTTGAGACTTAGTT	1111
Db	257	TTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTTTATTTTTTTTTTTTTTTTTTTTATTT	200

RESULT 8
US-08-998-416-563
; Sequence 563, Application US/08998416

```

; PATENT NO. 925201
;
; GENERAL INFORMATION:
;
; APPLICANT:  philippsen, Peter
;
; APPLICANT:  Pohlmann, Rainer
;
; APPLICANT:  Steiner, Sabine
;
; APPLICANT:  Mohr, Christine
;
; APPLICANT:  Wendland, Jurgen
;
; APPLICANT:  Knechtle, Philipp
;
; APPLICANT:  Reblischung, Corinne
;
; TITLE OF INVENTION:  GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
;
; TITLE OF INVENTION:  AND USCS THEREOF
;
; NUMBER OF SEQUENCES:  1152

```



```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: No. 6239264artis Corporation
/ STREET: 3054 Cornwallis Road
/ CITY: Research Triangle Park
/ STATE: No. 6239264th Carolina
/ COUNTRY: USA
/ ZIP: 27709
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/998,416
/ FILING DATE: 24-DEC-1997
/ CLASSIFICATION: 435
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: CH 0016/97
/ FILING DATE: 31-DEC-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meigs, J. Timothy
/ REGISTRATION NUMBER: 38,241
/ REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 919-541-8587
/ TELEFAX: 919-541-8689
/ INFORMATION FOR SEQ ID NO: 563:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 740 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ ORIGINAL SOURCE:
/ ORGANISM: PAG1390RP
/ US-08-998-416-563

Query Match          3.0%; Score 42.4; DB 3; Length 740;
Best Local Similarity 49.1%; Pred. No. 0.11;
Matches 112; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

QY 814 ATTCACTCTATTATATACACCTGCTCTAGCTTATCAACGTAAGCAAGCTTGA 873
   |||||
Db 106 ATTTATGATTTTGTGACATTTTGTGACATGTGATGTTATAAATATATTTAA 165

QY 874 TTTTAAAGCTTAATGATTTTGATGTTCTTTTCATTCGTAATTCACCTACCGACTT 933
   |||||
Db 166 TATTAATTTATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 225

QY 934 CGGCATTGGAATTTTAAATAATTAATTTAGAGCTGATTTTGAATTTTTCAGCGGAA 993
   |||||
Db 226 TCCATTATTAATTTGTTAGATTAACATTAATTAATTAATTAATTAATTAATTA 285

QY 994 TTTATTTTCACGTATGTAAGTTTACCTATTAATTAATTTTCA 1041
   |||||
Db 286 TAAATATGTTCAATTTTAATGATTAATTCATTAACGTATTCGATATAA 333

RESULT 9
US-09-621-976-1972
/ Sequence 1972, Application US/09621976
/ Patent No. 6639063
/ GENERAL INFORMATION:
/ APPLICANT: Dumas Milne Edwards, J.B.
/ APPLICANT: Jobert, S.
/ APPLICANT: Giordano, J.Y.
/ TITLE OF INVENTION: ESTs and Encoded Human Proteins.
/ FILE REFERENCE: GENSET.054PR2
/ CURRENT APPLICATION NUMBER: US/09/621,976
/ CURRENT FILING DATE: 2000-07-21
/ NUMBER OF SEQ ID NOS: 19335
/ SOFTWARE: Patent.pm
/ SEQ ID NO 1972
```

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/ LENGTH: 570
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 92..340
/ NAME/KEY: sig_peptide
/ LOCATION: 92..325
/ OTHER INFORMATION: Von Heijne matrix
/ OTHER INFORMATION: score 3.70000004768372
/ OTHER INFORMATION: seq NULLAFFSSPSTS/TF
US-09-621-976-1972

Query Match          2.9%; Score 41.8; DB 4; Length 570;
Best Local Similarity 61.5%; Pred. No. 0.14;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 940 TTGAATTTTAAATAATTTTAGAGCTGATTTGATTTTTCAGCGGAATTTATT 999
   |||||
Db 390 TTGAATTTTAAATAATGATGTAATTTCTTAGAGATTTTTCACCGCTTGTGTTACA 449

QY 1000 TTCACGTATGTAAGTTTACCTATAAATTAATTTTCAGCGGAGT 1048
   |||||
Db 450 GACCCAATGTAATAATTAATAAATAATTTGCAATTTTCTACAGAAAT 498

RESULT 10
US-09-949-016-1448
/ Sequence 1448, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1448
/ LENGTH: 2748
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-1448

Query Match          2.9%; Score 41.8; DB 4; Length 2748;
Best Local Similarity 61.5%; Pred. No. 0.34;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 940 TTGAATTTTAAATAATTTTAGAGCTGATTTGATTTTTCAGCGGAATTTATT 999
   |||||
Db 2582 TTGAATTTTAAATAATGATGTAATTTCTTAGAGATTTTTCACCGCTTGTGTTACA 2641

QY 1000 TTCACGTATGTAAGTTTACCTATAAATTAATTTTCAGCGGAGT 1048
   |||||
Db 2642 GACCCAATGTAATAATTAATAAATAATTTGCAATTTTCTACAGAAAT 2690

RESULT 11
US-09-949-016-13190
/ Sequence 13190, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
```

; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13190
; LENGTH: 36154
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13190

Query Match 2.9%; Score 41.8; DB 4; Length 36154;
Best Local Similarity 61.5%; Pred. No. 1.5;
Matches 67; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 940 TTGAATTTTAAATAATTTTAGAGCTGATTTTGTATTTTTCAGCGGAATTATT 999
DB 33988 TTGAATTTTAAATAATGATGGAATTTTAGAATTTTTCAGCGCTTGTTTACA 34047
QY 1000 TTCACGTATGTAAGTTTACCTATAATTAATTTTTCAGCGGAGT 1048
DB 34048 GACCCAATGTAATTAATAAATAATTAATTTTCAATTTTCTACAGAAAT 34096

RESULT 12

US-09-949-016-202462/c
; Sequence 202462, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202462
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-202462

Query Match 2.8%; Score 40.6; DB 4; Length 601;
Best Local Similarity 48.4%; Pred. No. 0.31;
Matches 109; Conservative 1; Mismatches 115; Indels 0; Gaps 0;

QY 40 ATAATACAAGTGTCTATGATTCAAAATTTGTCCTACAATATAAACAATTCAGCATGA 99
DB 347 ATACAAAAGCATCTTGACATATATTAGGTGCTCACTAAATGTAACYAGCATATTATTA 288
QY 100 AATCATACATTAATTTTCAGCTAATCAGATGCTTGAGGAGGAAAAATCTAAGCATTCAA 159
DB 287 GATACAAAATTAACATTTGAGTACAGGAGTTAGCAGTTTACAAAATATTTTATGTATA 228
QY 160 TATGCAAAAATTGATCACTGAAGTAACTGAAGAATATCTGTTTAAACATTAGTGT 219
DB 227 AGAGTATATGTAATTTTATGAATTAATTAAGTATTAATTAATTAATTAAGTGT 168
QY 220 AGTATTTATTAACAACATAAAATTTGTTATATTTTAGTACAAA 264
DB 167 AATTTTCAGAAAAAAGTAAATATACAGGCAATCTTAAGCACACA 123

RESULT 13

US-09-056-075-1
; Sequence 1, Application US/09056075
; Patent No. 595368
; GENERAL INFORMATION:
; APPLICANT: Johnson, Eric A.
; APPLICANT: Bradshaw, Marile
; APPLICANT: Rood, Julian
; TITLE OF INVENTION: Expression System for Clostridium
; TITLE OF INVENTION: Species
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Plinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (oriT) from
; OTHER INFORMATION: plasmid RP4"
US-09-056-075-1

Query Match 2.8%; Score 40.4; DB 2; Length 6243;
Best Local Similarity 49.1%; Pred. No. 1.3;
Matches 107; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 40 ATAATACAAGTGTCTATGATTCAAAATTTGTCCTACAATATAAACAATTCAGCATGA 99
DB 1227 ATAAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAAT 1286
QY 100 AATCATACATTAATTTTCAGCTAATCAGATGCTTGAGGAGGAAAAATCTAAGCATTCAA 159
DB 1287 AAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATA 1346
QY 160 TATGCAAAAATTGATCACTGAAGTAACTGAAGAATATCTGTTTAAACATTAGTGT 219
DB 1347 AATATATAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAAATATAAAAA 1406
QY 220 AGTATTTATTAACAACATAAAATTTGTTATATTTTA 257
DB 1407 TTTTATTTTAAAGTTGAAAAAAATTTTATATTTA 1444

RESULT 14
US-09-949-016-16065

```

; Sequence 16065, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16065
; LENGTH: 212139
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16065

```

	Query Match Best Local Similarity	2.8%; Score 40.4; DB 4; Length 212139;
	Matches 116; Conservative	0; Pred. No. 10; Mismatches 126; Indels 0; Gaps 0;
QY	810 ATGATTCACTGTATTTTATATACACCCTCCTCTAGCTTAACAAGTCCAAACT	869
DW	51215 ACCCACCATCCTCTGTATACGTTAATCATCTCTAGCTTACTATAATACCTAATACA	51274
QY	870 TGAATTTTAAAGCTTAAATTGATTTTGATGTTCTTTTCATCGTAATTCACCTAACGCACCT	929
DW	51275 ATCAAATGCTGTGTAATAATAGCTATTAATATGATTTTTTATTGGTAATATTTTATATTGTT	51334
QY	930 TAGTCGCATTTGAATTTTAAAAATAATTTTAGAGCTGATTTGATTTTTTTTCACG	989
DW	51335 TTGTGTGTTTTTAAATTTTTTTCCTGAATATATATGTGTGTGTATTTAGAGATGTTACTTT	51394
QY	990 GGAATTTATTTTCACGATGTATAAAGTTTAACTATAATTAATTTTCAGCGGAGTA	1049
DW	51395 GTGATTTTAATGTAAATTCAGAATAAACCTGTTAAGCATTTATTTTCTGTTTGTAGTAGCATTA	51454
QY	1050 AG 1051	
DW	51455 AG 51456	

```

RESULT 15
US-09-949-016-87645
; Sequence 87645, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 87645
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-87645

```

Query Match	2.8%	Score 40	DB 4	Length 601
Best Local Similarity	49.1%	Pred. No. 0.46		
Matches 106	Conservative 0	Mismatches 110	Indels 0	Gaps 0
QY	881	GCTTAATTGATTTGATGTTCTTTTCATGCTTAATCACTTACCGACCTTAGTCGCATT	940	
	203	GCTTAACCTTCGCCCTGGAATCTTTTGCTATCCCTGTCTTACTGTCTTAAATGAGCCT	262	
QY	941	TGAATTTTAAATAATTTTGTAGAGCTGATTTGATTTTTCAGCGAAATTATTT	1000	
	263	TTCTTATTGATACTATTATATATACTTGCCCTGCCTCCTTTTGTAGACAATTATTT	322	
QY	1001	TCACGTATGTAAGAATTTTACCTATAAATTATTAATTTTCAGCGAGTAAGCAATTACTGT	1060	
	323	TCATATTGTGTAATTAACAACGACACACAGCTTCTACACTTATGGGGTTCCCTTTCGGCA	382	
QY	1061	TATGGGTATAATCATCTGCTATGCTTAATCTCTT	1096	
	383	GAATGGGGCTGGTGACAAATTAATGACAGAAACTTTT	418	

Search completed: September 23, 2005, 19:24:03
Job time : 205 secs

Query Match	2.8%	Score 40	DB 4	Length 601
Best Local Similarity	49.1%	Pred. No. 0.46		
Matches 106	Conservative 0	Mismatches 110	Indels 0	Gaps 0
QY	881	GCTTAATTGATTTGATGTTCTTTTCATGCTTAATCACTTACCGACCTTAGTCGCATT	940	
	203	GCTTAACCTTCGCCCTGGAATCTTTTGCTATCCCTGTCTTACTGTCTTAAATGAGCCT	262	
QY	941	TGAATTTTAAATAATTTTGTAGAGCTGATTTGATTTTTCAGCGAAATTATTT	1000	
	263	TTCTTATTGATACTATTATATATACTTGCCCTGCCTCCTTTTGTAGACAATTATTT	322	
QY	1001	TCACGTATGTAAGAATTTTACCTATAAATTATTAATTTTCAGCGAGTAAGCAATTACTGT	1060	
	323	TCATATTGTGTAATTAACAACGACACACAGCTTCTACACTTATGGGGTTCCCTTTCGGCA	382	
QY	1061	TATGGGTATAATCATCTGCTATGCTTAATCTCTT	1096	
	383	GAATGGGGCTGGTGACAAATTAATGACAGAAACTTTT	418	

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Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1	CATTGAGAAATCATCTCCAGCCCTACAAATGTA	CTCTCCCATATACAGTGTCTCTATGA	60
QY	61	TTCAAAATTTGCTCTACAATATAAACATTTCCAGCATGAAATCCATACATTAATTTTCAG	120	
-Db	61	TTCAAAATTTGCTCTACAATATAAACATTTCCAGCATGAAATCCATACATTAATTTTCAG	120	
QY	121	CTAATCAGATGCTTGAGAGGGAATAATCTAAGCATTCATATATGCAAAATTTGATCACTGA	180	
Db	121	CTAATCAGATGCTTGAGAGGGAATAATCTAAGCATTCATATATGCAAAATTTGATCACTGA	180	
QY	181	AGTAAGTGAAGAGAAATATCTCGTTTAACTTAAGTCTAGTATTTATTAACAACACTAA	240	
Db	181	AGTAAGTGAAGAGAAATATCTCGTTTAACTTAAGTCTAGTATTTATTAACAACACTAA	240	
QY	241	AAATGTTTATATTTAGTACAATCGATAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300	
Db	241	AAATGTTTATATTTAGTACAATCGATAGTAGCAGTAGCAGAGCTAGCGTAAGATCG	300	
QY	301	TGTTCCGATCAGCTGAGAAACCGTCAGGTGTTGTCTGTGCCGTCCAGCCGATCAGAAAT	360	
Db	301	TGTTCCGATCAGCTGAGAAACCGTCAGGTGTTGTCTGTGCCGTCCAGCCGATCAGAAAT	360	
QY	361	TCGAGATCCGCGCTGTTCTTCTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAG	420	
Db	361	TCGAGATCCGCGCGTCTTCTTCTCTGAAATCTGCAAGTCCAGACAGCAGCAGCAGCAG	420	
QY	421	AGCAAGAGCAATGGCGTGACAGGAGTTTGATCTTGATGCACTAGCTAGCTACTAGCGC	480	
Db	421	AGCAAGAGCAATGGCGTGACAGGAGTTTGATCTTGATGCACTAGCTAGCTACTAGCGC	480	
QY	481	TTGCTTCCATGTCGCTCTCACGCCGTCGCAATGTGCCATGATCCTGCAATGCAATCAGCC	540	
Db	481	TTGCTTCCATGTCGCTCTCACGCCGTCGCAATGTGCCATGATCCTGCAATGCAATCAGCC	540	
QY	541	AAAGATTATATTTCTGACATTTTCTTCTCTATCGCTCCTAGTCGTCGTTTGGAGCTTA	600	
Db	541	AAAGATTATATTTCTGACATTTTCTTCTCTATCGCTCCTAGTCGTCGTTTGGAGCTTA	600	
QY	601	AAATTATGAAAAAGCAGCTGCTGAGAGCTAGCTGTGAGAAATCTGAAGATTGAGTTCT	660	
Db	601	AAATTATGAAAAAGCAGCTGCTGAGAGCTAGCTGTGAGAAATCTGAAGATTGAGTTCT	660	
QY	661	ACGTCATTTCTCCAGATTTCTACAAATTAACAGATTCTTATATTTAGTAAAAAGCTGACT	720	
Db	661	ACGTCATTTCTCCAGATTTCTACAAATTAACAGATTCTTATATTTAGTAAAAAGCTGACT	720	
QY	721	GTTTGGAGCTTCTGTCAAGCCGAGATTTCTGTGAGAAAGCTGCAGCTGTGAGAAGCTTCCC	780	
Db	721	GTTTGGAGCTTCTGTGTCAAGCCGAGATTTCTGTGAGAAAGCTGCAGCTGTGAGAAGCTTCCC	780	
QY	781	CAACAGACCCCTAGTGTACTCTAGCTGATGATTCACCTATTTATATACACCTTGC	840	
Db	781	CAACAGACCCCTAGTGTACTCTAGCTGATGATTCACCTATTTATATACACCTTGC	840	
QY	841	TCTCTAGCTTATCAACAGTAGCCAGACTTGAATTTTAAAGCTTAAATGATTTTGATGT	900	
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Db	901	TCTTTTCATCGTAATTCACCTTACCGACCTTAGTCGGCATTTGAATTTTAAAAATAATTT	960	
QY	961	TTAGAGCTGATTTGATTTTTTTTTCAGCGGAATTTATTTTCAAGTATGTAAGTTT	1020	
Db	961	TTAGAGCTGATTTGATTTTTTTTTCAGCGGAATTTATTTTCAAGTATGTAAGTTT	1020	
QY	1021	CCTATAAATTAATTTTTCAGCGGAGTAGAATTAAGTGTATGGGTTAATCATCTGG	1080	
Db	1021	CCTATAAATTAATTTTTCAGCGGAGTAGAATTAAGTGTATGGGTTAATCATCTGG	1080	

QY	1081	TATGCTTAAATCTCTTTACTTGGACTTAGTTGGGCAATTCGTAATGCATTCTCGTGCCA	1140	
Db	1081	TATGCTTAAATCTCTTTACTTGGACTTAGTTGGGCAATTCGTAATGCATTCTCGTGCCA	1140	
QY	1141	TCTTATATATACGGCCCTGCTAGCTTTGCTCTGTATCTGCACAGAAGACTAGCTGGCAA	1200	
Db	1141	TCTTATATATACGGCCCTGCTAGCTTTGCTCTGTATCTGCACAGAAGACTAGCTGGCAA	1200	
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Db	1201	AGTCTCAAGGCGAACCCTCCATCTTCTCTTCCAGCTCTCCATGGCGCTCCCTGT	1260	
QY	1261	CGCATCGCCATCGCCATGGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTAAT	1320	
Db	1261	CGCATCGCCATCGCCATGGCTCTCATGCTGAGAGATATCCAGCATGCTGAATTAAT	1320	
QY	1321	TGACGATATCATCTCATCATCACTTGCAATTTCAACTTCTGATTTGTCAGACATGTTTA	1380	
Db	1321	TGACGATATCATCTCATCATCACTTGCAATTTCAACTTCTGATTTGTCAGACATGTTTA	1380	
QY	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTTGTCCTTATCAAGTGTCTCAACCTGG	1436	
Db	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTTGTCCTTATCAAGTGTGTCAACCTGG	1436	
RESULT 2				
BD242727				
LOCUS				
DEFINITION				
ACCESSION				
VERSION				
KEYWORDS				
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AUTHORS				
TITLE				
JOURNAL				
COMMENT				
FEATURES				
ORIGIN				
Query Match				
Best Local Similarity				
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	1	CATTGAGAAATCATCTCCAGCCCTACAAATGTA	CTCTCCCATATACAGTGTCTCTATGA	60

OY 61 TTCAAAATTTGTCCTACATATTAACATTTCAGCATGAAATCCATACATTAATTTTCAG 120
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Db 61 TTCAAAATTTGTCCTACATATTAACATTTCAGCATGAAATCCATACATTAATTTTCAG 120
OY 121 CTAATCAGATGCTTGAGGGAATAATCTAAGCGATTCAATATGCAAAAATGATCACTGA 180
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OY 241 AAATGTTTATTTTATAGTACAATCGAGTAGAGCAAGACAGCTAGCGTAAGATCG 300
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Db 241 AAATGTTTATTTTATAGTACAATCGAGTAGAGCAAGACAGCTAGCGTAAGATCG 300
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OY 361 TCGAGATCCGCCGTCGTTCTTCTCGAAATCTGCAATGCCAGACAGACAGACAG 420
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OY 421 AGCAAGAGCAATGGCGTGAGGGAAGTTGATACCTTGATGCACTAGCTAGTACTAGCG 480
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Db 421 AGCAAGAGCAATGGCGTGAGGGAAGTTGATACCTTGATGCACTAGCTAGTACTAGCG 480
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Db 481 TTCGTTCCATGTGCTCTCAACGCCGTCGCAATGTGCCATGTCTGCATGCATCTGCC 540
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OY 601 AAATTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAGAATCTGAAGAATTGAGTCT 660
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Db 601 AAATTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAGAATCTGAAGAATTGAGTCT 660
OY 661 ACGTTCATCTCCAGATCTACAATTAACAGATTTCTATAATTTAGTAAAGCTGGA 720
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Db 721 GTTTGGAGCTTCTGTGTACGCCGAGAGATTCTGTGAGAACTGCAAGCTGTAGAACCTTCCC 780
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Db 781 CAAACAGACCCCTAGTGTACTCTAGCTGATGCATTCATCTATTATTAATACACTTGC 840
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Db 841 TCTCTAGCTTATCAAAAGTAGCCCAAGACTTGAATTTTAAAGCTTAAATGATTTGATGT 900
OY 901 TCTTTTCATCGTAATCACTTACCGACCTTAGTCGGCATTTGAATTTTAAATAATATT 960
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Db 901 TCTTTTCATCGTAATCACTTACCGACCTTAGTCGGCATTTGAATTTTAAATAATATT 960
OY 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTTTACCGTATGTAAAGTTTAA 1020
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Db 961 TTAGAGCTGATTTGATTTTTCAGCGGAATTTTACCGTATGTAAAGTTTAA 1020
OY 1021 CCTATAATTAATTTTACCGGAGTAGAGCATTAGTATGGGTATTAATCATCTGG 1080
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Db 1021 CCTATAATTAATTTTACCGGAGTAGAGCATTAGTATGGGTATTAATCATCTGG 1080
OY 1081 TATGCTTAATCTCTTAAGTGAAGTGAAGCAATTCGTAATGCAATCTCGTGCCA 1140
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Db 1081 TATGCTTAATCTCTTAAGTGAAGTGAAGCAATTCGTAATGCAATCTCGTGCCA 1140

OY 1141 TCTCTATAATACGGCCTGCTAGCTTTGCTCTGTATCTGACACACAAGAACTAGCTGGCAA 1200
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Db 1141 TCTCTATAATACGGCCTGCTAGCTTTGCTCTGTATCTGACACACAAGAACTAGCTGGCAA 1200
OY 1201 AGTCCCTCAAGGCGAAACCGCCTCATCTTCTCTTCCAGCTCTCCATGGCGTCCCTCGT 1260
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Db 1201 AGTCCCTCAAGGCGAAACCGCCTCATCTTCTCTTCCAGCTCTCCATGGCGTCCCTCGT 1260
OY 1261 CGCCATCGCCATCGCCATGCTCTCATGTGACAGATATCCAGCATGCTGAATTA 1320
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OY 1321 TGACGATATGATCTCATCATCATGCAATTTCAACTTCTGATTTGTCAGACATGTTTA 1380
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Db 1321 TGACGATATGATCTCATCATCATGCAATTTCAACTTCTGATTTGTCAGACATGTTTA 1380
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Db 1381 GCTGATCAGTAAACGTTGCCGTTGTAATGCTCTTATCAGGTGTTCAACCTGG 1436

RESULT 3
AP005392 145828 bp DNA linear PLN 28-JUL-2004
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,
DEFINITION PAC clone: P0463D04.
ACCESSION AP005392
VERSION AP005392.3 GI: 50725855
KEYWORDS
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
clone: P0463D04
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 145828)
AUTHORS Sasaki, T., Matsumoto, T. and Katayose, Y.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasakienias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Jul 27, 2004 this sequence version replaced gi:49169760.

COMMENT
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mlc.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), Genemark.hmm
(http://opal.biology.gatech.edu/Genemark/), Glimmer
(http://www.tigr.org/tdb/glimmer/glmr_form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.lasate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ. Protein homologies of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene

predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.
The orientation of the sequence is from SP6 to T7 of the PAC clone.
This sequence of P0463D04 has an overlap with P0463G11 (DBJ: AP005633) clone at 5' end and with OSJNBa0087J09 (DBJ: AC108761) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.afrc.go.jp/GenomeSeq.html>.

FEATURES

source

1. 145828
location/Qualifiers

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="9"

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/gene="P0463D04.1"

/note="hypothetical ORF

predicted by RiceHMM

this category is not included in IRGSP standard"

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/db_xref="GI:50725856"

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PEDYIIQRKRLIRLMIABGFIQKGTCSLEDAEGYLTVELVRSMIQVARNSENRIO
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LRTFLADTSMALSSASYFIFSESKYLAVLELSGLPIETIPIYSVGBLFNLRYLCINDT
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IYIQEGASLQYLIHIDSLMELRDVPTGIEFLRSVKEAYFTMMHSDFVRNLRTGKVAH
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/note="predicted by GeneMark.hmm etc."

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18801..20386

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18801..20386

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CDS

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18838..20235

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/gene="P0463D04.5"

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CDS

probably inactive due to including stop codon(s) in CDS

pseudogene, subcellular-like protein"

/pseudo

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/note="hypothetical ORF

predicted by GENSCAN

this category is not included in IRGSP standard"

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complement(31283..31731)

/gene="P0463D04.7"

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/note="contains full-length cDNA(s) : AK062866"

/codon_start=1

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predicted by Glimmer

this category is not included in IRGSP standard"

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/note="start and end point are not identified"

34608..35096

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similar to Oryza sativa chromosome 8, B1142B04.28"

/codon_start=1

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gene

misc_feature

gene

CDS

gene

mRNA

gene

misc_feature

mRNA

gene

CDS

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QY	61	TTCAAAATTTGTCCTACATATAAACATTTCCAGCAAGAATCCATACATTAATTTTCAG	120
Db	62946	TTCAAAATTTGTCCTACATATAAACATTTCCAGCAAGAATCCATACATTAATTTTCAG	63005
QY	121	CTAATCAGATGCTTGAGGGAATAATCTAAGCGATTCAATATGCCAAAATTGATCACTGA	180
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Db	63246	TCCGAGATCCGCCGCTCTTCTTCTCTGAATCTGCAAGTCCAGCAGCAGCAGCAG	63305
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QY	721	GTTTGGAGCTTCTGTCAAGCCGAGATTCTGTGAGAAAGCTGCAGCTGTGAGAGCTTCCC	780
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QY	781	CAAAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCACTCTATTTTATATACACCTTGC	840
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QY	901	TCTTTTCATCGTAATTCATTAACGACCTTAGTGGCAATTTGAATTTTAAAAATAATTT	960
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QY	961	TTAGAGCTGATTTGATTTTTTTTTCAGCGGAATTTATTTTCAGGTATGAAAGTTTTTA	1020
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QY	1021	CCTATAATATTAATTTTTCAGCGAGTAAGCAATTAAGTGTATGGGTTAATCATCTGG	1080
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RESULT 4
AP005633
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

154188 bp DNA linear PLN 15-SBP-2004
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 9,
PAC clone:P0463G11.
AP005633
AP005633.3 GI:50726137

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1
Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 9, PAC
clone:P0463G11
Published Only in Database (2002)
2 (bases 1 to 154188)
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (07-AUG-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgr.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
On Jul 27, 2004 this sequence version replaced gi:41152739.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), Genemark.hmm
(http://opal.biology.gatech.edu/Genemark/), Glimmer
(http://www.tigr.org/tdb/glimmer/glmr_form.html), RiceHMM
(http://rgr.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI NonRedundant Protein database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologues of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0463G11 has an overlap with P0556A05 (DDBJ: AP005759) clone at 5' end and with P0463D04 (DDBJ: AP005392) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/Genomeseq.html>.

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CDS

gene

mRNA

misc_feature

gene

mRNA

CDS

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mRNA

CDS

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Matches 1409; Conservative 0; Mismatches 25; Indels 11; Gaps 8;

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RESULT 5
BD242729 1196 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION DNA containing rice anther-specific gene and transgenic plants
transformed thereby.
ACCESSION BD242729
VERSION BD242729.1 GI:33052499
KEYWORDS JP 2002528125-A/3.
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 1196)
AUTHORS An,G., Jeon,J.S., Chung,Y.Y. and Lee,S.
TITLE DNA containing rice anther-specific gene and transgenic plants
JOURNAL Patent: JP 2002528125-A 3 03-SEP-2002;
COMMENT SYNGENTA PARTICIPATIONS AG
OS Oryza sativa (rice)

PN JP 2002528125-A/3
PD 03-SEP-2002
PF 02-NOV-1999 JP 2000579761
PR 03-NOV-1998 KR 1998/46973,19-NOV-1998 KR 1998/50126 PI
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C12N15/09,A01H5/00,C07K14/415,C12N15/00
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and transgenic plants
CC thereby transformed
FH Key
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LOCUS
DEFINITION Oryza sativa anther-specific protein gene, complete cds.
ACCESSION AF042275
VERSION AF042275.1 GI:4091009
KEYWORDS
SOURCE
ORGANISM Oryza sativa
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Brhartoidae; Oryzaceae; Oryza.
REFERENCE
AUTHORS Jeon,J.-S., Chung,Y.-Y., Lee,S., Yi,G.H., Oh,B.G. and An,G.
TITLE Isolation and characterization of an anther-specific gene, RA8,
from rice (Oryza sativa L.)
JOURNAL Plant Mol. Biol. 39 (1), 35-44 (1999)
MEDLINE 99178792
PUBMED 10080707
REFERENCE
AUTHORS Jeon,J.-S., Chung,Y.-Y., Lee,S. and An,G.
TITLE Direct Submission
JOURNAL Submitted (11-JAN-1998) Life Science, Pohang University of Science
and Technology, Pohang 790-784, Republic of Korea
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Matches 1081; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 288 CATGCCAAGATTATATCTCACATTTTCTCTCTATCGCTCCTAGTCGTCGTTGG 347
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QY 654 GAGTTCTACGTTCATTTCTCAGATTTCTACAATTACAGATTCTTATATTAGTAAAG 713
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QY 1434 TGG 1436
Db 1188 TGG 1190

RESULT 7
BD242735 240 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
DNA containing rice anther-specific gene and transgenic plants
transformed thereby.
ACCESSION
BD242735
VERSION
BD242735.1 GI:33052505
KEYWORDS
JP 2002528125-A/9.
SOURCE
Oryza sativa
Oryza sativa
Oryza sativa

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Oryza sativa (rice)
PN JP 2002528125-A/9
PD 03-SEP-2002
PF 02-NOV-1999 JP 2000579761
PR 03-NOV-1998 KR 1998/46973,19-NOV-1998 KR 1998/50126 PI
GYNHEUNG AN,JONG SEONG JEON,YONG YOON CHUNG,SICHUL LEE PC
C12N15/09,A01H5/00,C07K14/415,C12N15/00
CC DNA containing rice anther-specific gene
and transgenic plants
CC CC thereby transformed
CC CC Key Location/Qualifiers
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Db 61 TCGTGGCCATGCCATGCCATGGCTCTCATGCTGAGAGATATCCAGCATGCTGAATT 120
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Db 121 AACTGACGATATCATCTCATCATCACTTGCAATTTCAACTTCTGGAATGTCAGACATG 180
QY 1377 TTAGCTGATCAGTAAACGTTGCCGTTGTAATGTTCCCTTATCAGGTGTTCAACCTGG 1436

Db 181 TTAGCTGATCAGTAAACGTTGCCGTGTGAATTGCTCCTATCAGGTGGTTCAACCTGG 240

RESULT 8
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LOCUS Oryza sativa (japonica cultivar-group) cDNA clone:002-156-F12, full
DEFINITION insert sequence.
ACCESSION AK109240 GI:32994449
VERSION AK109240.1 GI:32994449
KEYWORDS FLI_CDNA; oligo capping.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS 1
The Rice Full-length cDNA Consortium, National Institute of
Agrobiological Sciences Rice Full-length cDNA Project Team;
Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K.,
Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I.,
Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C.,
Ohtsuki,K., Shishiki,T., Foundation of Advancement of International
Science Genome Sequencing & Analysis Group; Otsuo,Y., Murakami,K.,
Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y.,
Kurosaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M.,
Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., NIKURA,J.,
Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J.,
Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN;
Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,
Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
Yoshino,M. and Hayashizaki,Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
japonica rice
JOURNAL Science 301 (5631), 376-379 (2003)
MEDLINE 22752273
PUBMED 12869764

TITLE 2 (bases 1 to 598)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K.,
Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W.,
Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Hiraoka,T.,
Hori,F., Hotta,I., Iida,J., Iida,Y., Ikeda,R., Imamura,K.,
Imotani,K., Ishibiki,J., Ishii,Y., Ishikawa,M., Itoh,M., Kagawa,I.,
Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M.,
Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M.,
Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M.,
Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A.,
Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M.,
Namiki,T., Narikawa,R., NIKURA,J., Nishikawa,M., Nomura,K.,
Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H.,
Osato,N., Ota,Y., Otsuo,Y., Ryu,R., Saitoh,H., Sakai,C., Sakai,K.,
Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K.,
Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S.,
Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y.,
Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A.,
Toya,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W.,
Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and
Yoshimura,A.

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
COMMENT This clone is one of the 28K full-length cDNA clones from japonica
rice.
URL : http://cdna01.dna.affrc.go.jp/cdna/
NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,

Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group; Otsuo,Y., Iida,Y.,
Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,R., NIKURA,J., Oka,M., Ryu,R., Sugano,S.,
Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S.,
Yoshimura,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
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Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F.,
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Yasunishi,A. and Hayashizaki,Y.
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RESULT 9
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LOCUS OSJN00063 127952 bp DNA linear PLN 10-FEB-2004
DEFINITION Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNB0086G13,
complete sequence.
ACCESSION AL606706 GI:32480089
VERSION AL606706.3 GI:32480089
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS 1
Fu,G., Wang,S.Y., Ren,S.X., Lv,G., Lin,W., Gu,W.Q., Zhu,G.F.,
Tu,Y.F., Jia,J., Yin,H.F., Zhang,Y., Cai,Z., Chen,J., Kang,H.,
Chen,X.Y., Shao,Y., Sun,Y., Hu,Q.P., Zhang,X.L., Zhang,W.,

Wang,L.J., Ding,C.W., Sheng,H.H., Gu,J.L., Chen,S.T., Ni,L.,
Zhu,F.H., Han,B., Feng,Q., Huang,Y.C., Li,Y., Zhu,J.J., Zhao,Q.,
Hu,X., Liu,Y.L., Mu,J., Yu,Z., Chen,L., Fan,D.L., Weng,Q.J.,
Zhang,L., Lu,Y.Q., Yu,S.L., Liu,X.H., Lu,T.T., Zhang,Y.Y.,
Li,C., Li,T., Zhang,Y., Hu,H., Jia,P.X., Qian,Y.M., Ying,K.,
Zhou,B., Chen,Z.H., Hao,P., Zhang,L., Wu,M., Zhang,R.Q., Guan,J.P.
and Hong,G.F.

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bhan@ncgr.ac.cn

Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSJNB0086G13.
On Jul 8, 2003 this sequence version replaced gi:21741205.
Web site: http://www.ncgr.ac.cn

----- Summary Statistics -----
Assembly program: phrap

This is a complete sequence.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (http://www.softberry.com/),
genscan (http://CCR-081.mit.edu/GENSCAN.html), GenMarkESM
(http://genemark.biology.gatech.edu/Genemark/), tRNAscan-SE (Sean
Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE/), searches of the
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(ftp://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
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RESULT 10	OSJN00050/c	OSJN00050	156002 bp	DNA	linear	PLN 10-FEB-2004
LOCUS						
DEFINITION		Oryza sativa genomic DNA, chromosome 4, BAC clone: OSJNBa0088K19,				
ACCESSION		complete sequence.				
VERSION		AL606626				
KEYWORDS		AL606626.3	GI:32488551			
SOURCE		HTG.				
ORGANISM		Oryza sativa (japonica cultivar-group)				
		Oryza sativa (japonica cultivar-group)				
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
		Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				

REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCES AUTHORS
----------------------	--

Ehrhartoideae; Oryzeae; Oryza.

1
Feng, Q., Zhang, Y., Hao, P., Wang, S., Fu, G., Huang, Y., Li, Y., Zhu, J.,
Liu, Y., Hu, X., Jia, P., Zhang, Y., Zhao, Q., Ying, K., Yu, S., Tang, Y.,
Weng, Q., Zhang, L., Lu, Y., Mu, J., Lu, Y., Zhang, L. S., Yu, Z., Fan, D.,
Liu, X., Lu, T., Li, C., Wu, Y., Sun, T., Lei, H., Li, T., Hu, H., Guan, J.,
Wu, M., Zhang, R., Zhou, B., Chen, Z., Chen, L., Jin, Z., Wang, R.,
Yin, H., Cai, Z., Ren, S., Lv, G., Gu, W., Zhu, G., Tu, Y., Jia, J.,
Zhang, Y., Chen, J., Kang, H., Chen, X., Shao, C., Sun, Y., Hu, Q.,
Zhang, X., Zhang, W., Wang, L., Ding, C., Sheng, H., Gu, J., Chen, S.,
Li, J., Hong, G., Xue, Y., Lan, L., Lai, Y., Cheng, Z., Gu, M., Jiang, J.,
Sequence and analysis of rice chromosome 4
Nature 420 (6913), 316-320 (2002)
22337377
12447439

TITLE
JOURNAL

REMARK

COMMENT

Submitted (08-SEP-2001) Han Bin, National Center for Gene Research,
Chinese Academy of sciences, 500# Cao Bao Road, Shanghai 200233,
CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSUNBa0088X19.
On Jul 9, 2003 this sequence version replaced gi:21740748.
Web site: <http://www.ncgr.ac.cn>
----- Summary Statistics -----
Assembly program: phrap

This is a complete sequence.
Genes were identified by a combination of several methods: Gene
prediction programs including Fgenesh (<http://www.softberry.com/>),
GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), GenemarkHM
(<http://genemark.biology.gatech.edu/Genemark/>), tRNAscan-SF (Sean
Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SF/>), searches of the
complete sequence against NCBI none redundant protein database (nr)
(<ftp://ncbi.nlm.nih.gov/blast/db>) and the BSR database at NCGR.

FEATURES

Source

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CDS

CDS

gene

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Best Local Similarity 82.1%; Pred. No. 2.9e-21;
Matches 183; Conservative 0; Mismatches 37; Indels 3; Gaps 2;
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QY 645 GAAGAATTGAGTTCTACGTTCAATTCAGATTCTACAATTACAGATTCTTATAATTTA 704
Db 149847 GGAGAAGCTGCTTCTA-GTTCATTTCCAGATTTTACAACTACAGATTCTCAGAATCTG 149789
QY 705 GGTAAAAAGCTGAGCTGTTT--GGAGCTTCTGTCAAGCCGAGATTCGTGAGAAGCTGC 762
Db 149788 GGTAAAAAGCTGAGCTGTTTGGGGAGCTTCTAGCAACTGAGAGATTCTAGAGAAGCTGC 149729
QY 763 AGCTGCTAGAGCTTCCCCAACAAGACCCCTAGTTGTAATCTA 805
Db 149728 AGCTGCTAGAGCTCCCCAACAAGCCAGACTCTGTTCCCAA 149686
RESULT 11
AP005106/c 126544 bp DNA linear PLN 22-JUL-2004
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 7,
DEFINITION BAC clone:OSJNBb0091119.
ACCESSION AP005106
VERSION AP005106.6 GI:50510301

KEYWORDS

SOURCE ORGANISM

Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; *Oryza*.

REFERENCE

AUTHORS
TITLE

JOURNAL REFERENCE

TITLE
JOURNAL

COMMENT

On Jul 22, 2004 this sequence version replaced gi:34395386. Genes were predicted from the integrated results of the following: GENSCAN (<http://CCR-081.mit.edu/GENSCAN.html>), FGENESH (<http://www.softberry.com/>), Genemark.hmm (<http://opal.biology.gatech.edu/Genemark/>), GlimmerM (http://www.tigr.org/cdb/glimmerm/glm_form.html), RiceHMM (<http://rpg.dna.affrc.go.jp/RiceHMM/>), SplicePredictor (<http://bioinformatics.iastate.edu/cgi-bin/sp.cgi>), sim4 (<http://globin.cse.psu.edu/html/docs/sim4.html>), gap2 (<http://www.tigr.org/software/glimmer/>), BLASTN and BLASTX. The genomic sequence was searched against NCBI NonRedundant Protein database, nr (<ftp://ncbi.nlm.nih.gov/blast/db>) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of OSUNB0091119 clone has an overlap with OSUNBA0028021 (DDBJ: AP005766) clone at 5' end and with P0045F02 (DDBJ: AP004268) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rpg.dna.affrc.go.jp/GenomeSeq.html>.

FEATURES

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Location/Qualifiers
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/mol_type="genomic DNA"

/cultivar="Nippobare"

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1669. .8396

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PROBABLY INACTIVE due to including BOP CODON(8) IN CBS

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CDS	join(29573. .29674,35129. .35485) /gene="OSJNB0091119.111" /note="predicted by Genemark.hmm etc." /codon_start=1 /product="hypothetical protein" /protein_id="BAC22413.1" /db_xref="GI:24414170" /translation="MPRGREQHNDASPTLCROAGKATPKPSTPRWLDEYQAAEGAQV LRAGRNRWGGGGSDDDGCTAATVAITGLMAARREVIGEAKDVAVGDEADAAAVA VAGQGTATRCGCGGGGRSGGCGATCVRDALDHRCRVHPVGSDDDG"
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QY	696 TATTAATTAGTAAAAAGCTGACTGTTT--GGGAGCTTCTGTCAAGCCGGAGATTCTGT 752 Db 72351 CCGAATTTGGTAAAAAGCTGAGTTGTTGGGGGAGCTTTCAGCAACTGAGATTCTAG 72292
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RESULT 12
AC144738/c

LOCUS	AC144738 156649 bp DNA linear PLN 22-JUL-2004
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 5 clone
ACCESSION	OSJNBa0029B02, complete sequence.
VERSION	AC144738
KEYWORDS	AC144738.2 GI:40385890
SOURCE	HTG.
ORGANISM	Oryza sativa (japonica cultivar-group)
REFERENCE	Oryza sativa (japonica cultivar-group) Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza. 1 (bases 1 to 156649) Chow,T.-Y., Hsing,Y.-I.C., Chen,C.-S., Chen,H.-H., Liu,S.-M., Chao,Y.-T., Chang,S.-J., Chen,H.-C., Chen,S.-K., Chen,T.-R., Chen,Y.-L., Cheng,C.-H., Chung,C.-I., Han,S.-Y., Hsiao,S.-H., Hsiung,J.-N., Hsu,C.-H., Huang,J.-J., Kau,P.-I., Lee,M.-C., Liu,H.-L., Li,Y.-F., Lin,S.-J., Lin,Y.-C., Wu,S.-W., Yu,C.-Y., Yu,S.-W., Wu,H.-P. and Shaw,J.-F. Oryza sativa BAC OSJNBa0029B02 genomic sequence
TITLE	Unpublished
REFERENCE	2 (bases 1 to 156649) Chow,T.-Y. and Hsing,Y.-I.C. Direct Submission Submitted (15-MAY-2003) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan 3 (bases 1 to 156649) Chow,T.-Y. Direct Submission Submitted (30-DEC-2003) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan 4 (bases 1 to 156649) Chow,T.-Y. and Hsing,Y.-I.C. Direct Submission Submitted (22-JUL-2004) Institute of Botany, Academia Sinica, 128, Section 2, Academia Road, Nankang, Taipei 11529, Taiwan On Dec 30, 2003 this sequence version replaced GI:30725893. Genes were predicated from the integrated results of the following: BLASTN2.0, BLASTX2.0, GENSCAN (Chris Burge, http://genes.mit.edu/GENSCAN.html), Fgenesh (http://www.softberry.com/), GlimmerX (http://www.tigr.org/softlab/glimmer/glimmer.html), TWINSKAN (http://genes.cs.wustl.edu/) and Gensplicer (http://www.tigr.org/tdb/Gensplicer/index.shtml). The sequence was searched against the Swiss-Prot+TrEMBL protein database, the NCBI Plant EST database, the TIGR Rice Gene Index and the rice full-length cDNA database (KOME http://cdna01.dna.affrc.go.jp/cDNA/). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. This clone overlaps with P0617A08(accession # AC135426) and P0478F09(accession # AC130610).
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CDS		complement (join(36810..36927,37068..37228,38000..38071, 39555..39788,39919..39982,40096..40145,40248..40355)) /gene="OSJNBa0029B02.5" /note="similar to rice EST CF328929, AK099352"
	gene	/codon_start=1 /product="unknown protein" /protein_id="AAU77344.1" /db_xref="GI:50511421"
CDS		/translation="MMRAWAAGMLRRASGEASLARAVFARGFLGLNMKASKETIE KKSKDKARLMDMSRGYFADIAIRKNGGKLATANKIIPAIKVPFDLSVKSPPDGR TVNLPLVAPFRNDPOTGTNTVDTONDCAGDMVYPDASIVCLSFASQKAEWTL PFUDAFSSAGNIQVEYSFIDSWLSSPVROVFLKVMTKSNMPORHAYTAFGDHYTF RKLHLINLLTGTYLYVDRIGRVRWQGFSAIQEELSLTACTSILLDGK" 40643..41054 /gene="OSJNBa0029B02.6" /note="unknown protein" join(40643..40686,40759..40856,40960..41054) /gene="OSJNBa0029B02.6" /note="similar to rice EST CF335454, AK071760"
	gene	/codon_start=1 /product="unknown protein" /protein_id="AAT77345.1" /db_xref="GI:50511422"
CDS		/translation="MASAASSSSSTQPDAAARQQQLQQQRKPPLIMLPLIYAPV LPRI RIGLRHPNPMWRDLFFGVLAGAFAGTYLM" complement (45034..45390) /gene="OSJNBa0029B02.7" /note="unknown protein" complement (45034..45390) /gene="OSJNBa0029B02.7" /note="similar to rice EST AK071729"
	gene	/codon_start=1 /product="unknown protein" /protein_id="AAT77346.1" /db_xref="GI:50511423"
CDS		/translation="MAMATSASTVSFSARPASAASAVRPCAAAGRARARAAGSGKM WAPLGWSGKADYIEAPAPVAVVAEESEARRRPVGLTEKARELRARVETESFH DAMYHSALIASRLARSA" complement (52389..59739) /gene="OSJNBa0029B02.8" /note="hypothetical protein" complement (join(52389..52454,54463..54597,55141..55408, 55896..56218,56563..56679,56776..56889,57080..57253,
Query Match	8.8%; Score 126; DB 8; Length 156649;	
Best Local Similarity	80.1%; Pred. No. 1.7e-18;	
Matches 173; Conservative	0; Mismatches 40; Indels 3; Gaps 2;	
QY	581 GTCGCTGTTGGGAGCTTAATAATTATGAAGAAGCAGCTGCTGAGAAGCTAGCTGGTGAGA	640
Db	84560 GGCCGTGTTGGGGAGGTTAAGATTCTGAAAAAGAGCTGCTAAGAAGCTAGCTGGTGAGA	84501
QY	641 ATCTGAAGAAATTGAGTTCACGTTCAITCTCCAGATTCTACAAATTACAGATTCTTATAA	700
Db	84500 AACCCAGC--TTCTGCGCTTCTAGTTTATTTTCTAGATTCTACAACTACAGATTCTTAGAA	84443
QY	701 TTTAGTAAAGAAAGCTGAGCTGTTGGG-AGCTTCTGTACGCCGAGATTCTGTGAGAAGC	759
Db	84442 TCTAGTAAGAAAAGCTGAGCTGTTGGGAAGCTTCTGCAACTGGAGATTCTAGAGAAGC	84383
QY	760 TGACAGCTGCTAGAAGCTTCCCCAACAAGACCCTAG	795

Db 84382 TGCAGTTGCTAGAGCTCCCAATAAGCCCTTAG 84347

RESULT 13
AP004323/c
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 6 clone
OJ118_C02, *** SEQUENCING IN PROGRESS ***.
ACCESSION AP004323
VERSION AP004323.1 GI:16930108
KEYWORDS HTG, HTGS, PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
clone:OJ118_C02
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 95209)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
Source
1. .95209
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="OJ118_C02"

ORIGIN
Query Match 8.5%; Score 121.6; DB 2; Length 95209;
Best Local Similarity 74.0%; Pred. No. 1.7e-17;
Matches 188; Conservative 0; Mismatches 49; Indels 17; Gaps 2;
OY 592 GGGAGCTTAAATATGAAAAGCAGCTGTGAGAGCTAGCTGGTGAAGATCGAAGAT 651
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DB 89229 GGGAGCTTAAGATTTCGAAAGCAGCTGTGAGAGCTAGCTGTGAAGATCGAAG 89170
|||||
OY 652 TTGA-----GTTCTAGCTTCATTCACAGATTCTACAATTACAGATTCTT 696
|||||
DB 89169 CTGGAACCCAGCTTCTGGCTTCTAGTTCATTTTCAGATTCTACACTACAGATTCTC 89110
|||||
OY 697 ATAATTAGTAAAGCTGGAAGCTGTT--GGAGCTTCTGTACGCCGAGATTCTGTGA 754
|||||
DB 89109 AGAATCTGGTAAAGCTGGAAGCTGTTGGGGAGCTTCTGACAACTGGAATTTCTAGTA 89050
|||||
OY 755 GAAAGCTGAGCTGTAGAAAGCTTCCCAACAGACCCCTAGTTGTACTCTAGCTGATCGA 814
|||||
DB 89049 GAAAGCTGAGCTGTAGAAAGCTTCCCAACAGACCCCTATATGACAACTTACTTCTCTT 88990
|||||
OY 815 TTCACTCTATTTTA 828
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Db 88989 TGGGCTGCACTTAA 88976

RESULT 14
AP005966/c
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
BAC clone:B1047H05.
ACCESSION AP005966
VERSION AP005966.3 GI:50726539
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
clone:B1047H05
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 187273)
AUTHORS Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE Direct Submission
JOURNAL Submitted (26-NOV-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT On Jul 27, 2004 this sequence version replaced gi:47971628.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmer/glmr_form.html), RiceHMM
(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein
database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA
sequence database at RGP or DDBJ. Protein homologes of the coding
regions were searched against NCBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Full-length cDNAs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no.
A gene with identity or significant homology to a protein is
classified based on the protein name to indicate the homology level
such as same name, 'putative-' and '-like protein'. A gene without
significant homology to any protein but with full-length cDNA or
EST homology (covering almost the entire length of partial
sequence) is classified as an 'unknown' protein. A gene predicted
by two or more gene prediction programs is classified as a
'hypothetical' protein according to IRGSP standard. A gene
predicted by a single gene prediction program is also classified as a
miscellaneous feature of the sequence.
The orientation of the sequence is from M13rev to -21M13 of the BAC
clone. This sequence of B1047H05 clone has an overlap with P0633E08
(DDBJ: AP003622) at 3' end. Detailed information on overlap and
assembly quality together with annotation of this entry is
available at http://rgp.dna.affrc.go.jp/Genomeseq.html.
FEATURES
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
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/chromosome="6"
/clone="B1047H05"
complement(327..2093)
/gene="B1047H05.1"

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                  /note="probably inactive due to 5' exon missing in CDS
                  pseudogene, GAG-POL precursor"
                  /pseudo
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                  4065. .4180)
                  /gene="B1047H05.2"
                  join(2836. .2984,3392. .3462,3591. .3666,3754. .3827,
                  4065. .4180)
                  /gene="B1047H05.2"
                  /note="hypothetical ORF
                  predicted by Genemark.hmm
                  this category is not included in IRGSP standard"
                  7570. .8024
                  /gene="B1047H05.3"
                  <7570. .>8024
                  /gene="B1047H05.3"
                  /note="supported by full-length cDNA(s) : AK062314"
                  7570. .8024
                  /gene="B1047H05.3"
                  /note="contains full-length cDNA(s) : AK062314
                  non-coding transcript
                  probably inactive due to including stop codon(s) in CDS"
                  complement(join(8076. .10056,10155. .11416))
                  /gene="B1047H05.4"
                  complement(join(8076. .10056,10155. .11416))
                  /gene="B1047H05.4"
                  /note="retrotransposon protein-like"
                  complement(11918. .13366)
                  /gene="B1047H05.5"
                  complement(join(<11918. .11979,12095. .12218,13015. .13123
                  13260. .>13366))
                  /gene="B1047H05.5"
                  /note="start and end point are not identified"
                  complement(join(11918. .11979,12095. .12218,13015. .13123,
                  13260. .13366))
                  /gene="B1047H05.5"
                  /note="similar to Oryza sativa chromosome 1, P0463F06.28"
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                  /protein_id="BAD34174.1"
                  /db_xref="GI:50726540"
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                  KQLKVTLEVAPHRETAQALCOFGRGLRCKPHKSGHLGPRGRSNPTPPRGNOEEG
                  GHLTLGPDVPEGKRSGMTPIKPGDRWDRSP"
                  complement(15812. .17991)
                  /gene="B1047H05.6"
                  complement(join(<15812. .15981,17970. .>17991))
                  /gene="B1047H05.6"
                  /note="start and end point are not identified"
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                  /gene="B1047H05.6"
                  /note="predicted by GENSCAN etc."
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                  /protein_id="BAD34175.1"
                  /db_xref="GI:50726541"
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                  GVIVIGGEHVVVQWTRITLM"
                  18451. .18813
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                  join(<18451. .18560,18678. .>18813)
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                  /note="start and end point are not identified"
                  join(18451. .18560,18678. .18813)
                  /gene="B1047H05.7"
                  /note="predicted by Genemark.hmm etc."
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                  /protein_id="BAD34176.1"
                  /db_xref="GI:50726542"
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mRNA	<20823. .>22640	/gene="B1047H05.8"	/note="start and end point are not identified"
CDS	20823. .22640	/gene="B1047H05.8"	/codon_start=1
		/product="putative disease resistance protein Cf-2.1"	
		/protein_id="BAD34177.1"	
		/db_xref="GI:50726543"	
		/translation="MSSLGFSRPGFLQLYLKFCCLPLVIGSNETESDRALLCLK	
		SQLTGSABVLSSWSNASMEFCSWGHVCTQYPRRVATLDLSEGITGSISPCIANLT	
		YLTKQLSNNSFYGSIPEBLGFLTQLSILNISMSLEGNPELTSFCFKQKIDISNN	
		KLQGSIPSAFGDLTELRTLILTSNRLSGDIPQSLGSNLSTLYVDLRNALAGRIPOS	
		ASSTSLQFLILTSNLSGELPKALINSSSLIFLDLQNNRYGSIIPVTAISPKMYLD	
		LRFNHLTGITPSSIGNLSSILTYKILGNLVGSIPTDIGHVPTLETIAVNNNLGSPV	
		PSIFENVTSILTYLGMANNSLTGRLPISNIGYTLPINIQILLPNKPSGSIPESSLNASH	
		LQRLFLTNNSFTGHIPEFGSLQNLLEIDMAYNMLBAGDMSFYSSLTNCCKLTQLLDG	
		MLQGNLPSCICGNLSSLSLEHLNRNMNISGLIPGIGNLNLTLYMDNLTGNIIP	
		TIGYLHNMKLYMDNYLTGNIPTGILHSWVFLSFNRLSGQIPGTIGNLVQVNE	
		LRIDENNLGSGIPASIRHCTQTLTKNLAHNSLHGTTIAS"	
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mRNA	<24538. .>24975	/gene="B1047H05.9"	
CDS	24538. .24975	/note="start and end point are not identified"	
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		/note="predicted by Glimmer etc."	
		/codon_start=1	
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		/db_xref="GI:50726544"	
		/translation="MDLEBGRGLERRBEGEPALSSVAASSSLTEPSSLVBLDGR	
		RLIACADGRLLFRRCSSRPLLAESDCCRLACANGRLILFRHRHRSWPLLAES	
		DGCRQLVCSNGHRLILFHSRHRCRLLARAKPTATGSSSR"	
gene	complement(26909. .27955)	/gene="B1047H05.10"	
mRNA	complement(join(<26909. .27047,27707. .27833,27868. .>27955))	/gene="B1047H05.10"	
CDS	complement(join(26909. .27047,27707. .27833,27868. .27955))	/gene="B1047H05.10"	
		/note="predicted by RiceHMM etc."	
		/codon_start=1	
		/product="hypothetical protein"	
		/protein_id="BAD34179.1"	
		/db_xref="GI:50726545"	
		/translation="MMRLFTTPSAKVAVLRAAVAVPMYGGSRADPEKVAHLDSIV	
		HVVNNPTPRHGHTGADKAAEAADPSESKPPLGSSGTCKTSHYKVVWTGAYMESA	
		SPMVSTVLRPARKII"	
gene	complement(30838. .31158)	/gene="B1047H05.11"	
mRNA	complement(<30838. .>31158)	/gene="B1047H05.11"	
CDS	/note="start and end point are not identified"		
	complement(30838. .31158)		
Query Match	8.5%; Score 121.6; DB 8; Length 187273;		
Best Local Similarity	74.0%; Pred.No.1.8e-17;		
Matches 188; Conservative	0; Mismatches 49; Indels 17; Gaps 2;		
QY	592 GGGAGCTTAAATATATGAAAGCAGCTGCTGAGAACTAGCTGGTGAATCTGAAGAAT 651		
Db	122593 GGGAGCTTAAGATTTTGAGAACAGCTGCTGAGAACTAGCTGGTGAATCTGAGAAAG 122534		
QY	652 TTGA-----GTTCTACGTTCAATCTCCAGATTCTACAATTAAGATTCTT 696		
Db	122533 CTGGAATAACCCAGCTTCTGGCTTCTAGTTCAATTTTTCAGATTCTACAATAAGATTCTC 122474		
QY	697 ATAATTAGCTAAAAAGCTGCACTGTTT--GGAGAGCTTCTGTACAGCCGAGAGATTCTGTGA 754		

Db 122473 AGAATCTGGGTAAGCTGACTGTTGGGGGAGCTTCTGACAACCTGAGATTCTAGTA 122414
QY 755 GAACTGCAGCTGCTAGAAAGCTTCCCAACAGACAGACCCCTAGTGTACTCTAGCTGATCGA 814
Db 122413 GAACTGCAGCTGCTAGAAAGCTTCCCAACAGAGCCCAATATGACAACCTACTCTCTCTT 122354
QY 815 TTCACCTCTATTTTA 828
Db 122353 TGGGCTGCAGTTAA 122340

RESULT 15

AP003625/c 134159 bp DNA linear HTG 21-MAR-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 6 clone P0701F09,
DEFINITION *** SEQUENCING IN PROGRESS ***.

ACCESSION AP003625 GI:14020963
VERSION AP003625.1 GI:14020963
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone: P0701F09
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 134159)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)

COMMENT
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
1. 134159
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="P0701F09"

ORIGIN

Query Match 8.4%; Score 120; DB 2; Length 134159;
Best Local Similarity 73.6%; Pred. No. 4.2e-17;
Matches 187; Conservative 0; Mismatches 50; Indels 17; Gaps 2;
QY 592 GGGAGCTTAAATTTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAGAATCTGAAGAAT 651
Db 57995 GGGAGCTTAAATTTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGAGAATCTGAGAAG 57936
QY 652 TTGA-----GTTCTACGTTTCATTCAGATTCTTCAATTAAGATTTCTT 696
Db 57935 CTGAAAACCCAGCTTCTGCTTCTAGTTTCATTTTTCAGATTCTACAACTACAGATTCTC 57876
QY 697 ATAATTTAGTAAAGCTGGAAGCTGTTT--GGAGCTTCTGTCAAGCCGAGATTCTGTGA 754
Db 57875 AGAATCTGGTAAAGCTGGAAGCTGTTTGGGGAGCTTCTGACAAGCTGAGATTCTAGTA 57816

QY 755 GAACTGCAGCTGCTAGAAAGCTTCCCAACAGACAGACCCCTAGTGTACTCTAGCTGATCGA 814
Db 57815 GAACTGCAGCTGCTAGAAAGCTTCCCAACAGAGCCCAATATGACAACCTACTCTCTCTT 57756
QY 815 TTCACCTCTATTTTA 828
Db 57755 TGGGCTGCAGTTAA 57742

Search completed: September 23, 2005, 18:23:22
Job time : 4320 secs

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XX 03-NOV-1998; 98KR-00046973.
PR 19-NOV-1998; 98KR-00050126.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI An G, Jeon J, Chung Y, Lee S;
XX
DR WPI; 2000-365632/31.
DR P-PSDB; AAY96273.
XX
PT Novel promoters of anther-specific transcription used to create
PT transgenic male-sterile plants.
XX
PS Claim 15; Page 28-29; 32pp; English.
XX
CC The present sequence is the gene regulator for the rice RA8 protein. This
CC protein is expressed in an anther-specific manner in the plant, where it
CC aids in the development of the structure. The gene can be used to create
CC transgenic plants which do not possess a properly formed anther, and thus
CC are male-sterile. This is useful as it prevents self-pollination, which
CC will then aid breeding and hybrid seed production. In addition to rice,
CC this process can also be used in wheat, maize, orchardgrass and Sorghum
CC bicolor
XX
SQ Sequence 1436 BP; 387 A; 313 C; 273 G; 463 T; 0 U; 0 Other;

Query Match 100.0%; Score 1436; DB 3; Length 1436;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTGAGATCATCTCCAGCCTACATGATCTCTCCCATATACAGTGTCTATGA 60
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QY 61 TTCAAATTTGCTCTACATATAAACATTTCCAGCATGAAATCCATATATTTTCA 120
DB 61 TTCAAATTTGCTCTACATATAAACATTTCCAGCATGAAATCCATATATTTTCA 120
QY 121 CTATCAGATGCTTGAGGAGAAATCTAAGCATTCATATGCAAAATGATCACTGA 180
DB 121 CTATCAGATGCTTGAGGAGAAATCTAAGCATTCATATGCAAAATGATCACTGA 180
QY 181 AGTAAGTGAAGAGATATCTGTTTAACTAGTCTAGTATTTTAACTAA 240
DB 181 AGTAAGTGAAGAGATATCTGTTTAACTAGTCTAGTATTTTAACTAA 240
QY 241 AAATGTTTATTTAGTAAATCGAGTAGACAGTAGAGAGCGTAAGATCG 300
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QY 301 TGTTCGATCACTGAGAAACCGTCAGGTGTTGTCTGTGCCGTCAGCGCATGAAT 360
DB 301 TGTTCGATCACTGAGAAACCGTCAGGTGTTGTCTGTGCCGTCAGCGCATGAAT 360
QY 361 TCGAGATCCGCGCTGTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAG 420
DB 361 TCGAGATCCGCGCTGTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAG 420
QY 421 AGCAAGAGCAATGGCGTGAGGAGGAGTTGATCTTGATGACACTAGCTAGCTA 480
DB 421 AGCAAGAGCAATGGCGTGAGGAGGAGTTGATCTTGATGACACTAGCTAGCTA 480
QY 481 TTGCTTCATGCTGCTCAAGCGCGTGAATGCGATGATCCTGCATGATCATCGCC 540
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QY 541 AAGATTATATCTCTACATTTTCTTCTCTATCGCTCTAGTGTGTTGGAGCTTA 600
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DB 601 AAATTATGAAAAGCAGCTGCTGAGAAAGCTAGCTGCTGAGAAATCTGAAGATTG 660

DB 601 AAATTATGAAAAGCAGCTGCTGAGAAAGCTAGCTGCTGAGAAATCTGAAGATTG 660
QY 661 ACGTTGATTTCTCCAGATTTCTACAAATTACAGATTCTTATATTTAGTAAAGCTG 720
DB 661 ACGTTGATTTCTCCAGATTTCTACAAATTACAGATTCTTATATTTAGTAAAGCTG 720
QY 721 GTTGGAGCTTCTGTGAGCCGAGATTCTGTGAGAAAGCTGAGCTGCTAGAGCTTCCC 780
DB 721 GTTGGAGCTTCTGTGAGCCGAGATTCTGTGAGAAAGCTGAGCTGCTAGAGCTTCCC 780
QY 781 CAAACAGACCCCTAGTGTGATCTGATGATGATGATGATGATGATGATGATGATG 840
DB 781 CAAACAGACCCCTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATG 840
QY 841 TCTCTAGCTTATCAAAAGCTAGCAGAGCTGAAATTTTAAAGCTTAAATTTGATGT 900
DB 841 TCTCTAGCTTATCAAAAGCTAGCAGAGCTGAAATTTTAAAGCTTAAATTTGATGT 900
QY 901 TCTTTTCATCGTAATTCATTCACGACCTTAGTGGCATTTGAATTTTAAATAATTT 960
DB 901 TCTTTTCATCGTAATTCATTCACGACCTTAGTGGCATTTGAATTTTAAATAATTT 960
QY 961 TTAGAGCTGATTTTGAATTTTCTTACGCGGAATTTATTTTCAAGTATGTAAGTTT 1020
DB 961 TTAGAGCTGATTTTGAATTTTCTTACGCGGAATTTATTTTCAAGTATGTAAGTTT 1020
QY 1021 CCTATAATTTATTTATTTTCAAGCGAGTAAGCATTTAGTGTATGCTTATCATCTGG 1080
DB 1021 CCTATAATTTATTTATTTTCAAGCGAGTAAGCATTTAGTGTATGCTTATCATCTGG 1080
QY 1081 TATGCTTAAATCTCTTACTTGACTTGTGGACAATTCGTAATGATCTCTGAGCA 1140
DB 1081 TATGCTTAAATCTCTTACTTGACTTGTGGACAATTCGTAATGATCTCTGAGCA 1140
QY 1141 TCTCTATAATACGGCCTGCTAGCTTGTCTTGTATCTGACACAGAACTAGCTGCAA 1200
DB 1141 TCTCTATAATACGGCCTGCTAGCTTGTCTTGTATCTGACACAGAACTAGCTGCAA 1200
QY 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTTCCAGCTCTCCCATGCGCTCGT 1260
DB 1201 AGTCTCAAGGCGAACCGCTCCATCTTCTCTTCCAGCTCTCCCATGCGCTCGT 1260
QY 1261 CGCCATGCGCATCGCCATGCGCTCTGATGCTGACAGAGATATCCAGATGCTGAATTA 1320
DB 1261 CGCCATGCGCATCGCCATGCGCTCTGATGCTGACAGAGATATCCAGATGCTGAATTA 1320
QY 1321 TGACGCATATCATCTCATCATCATCTTGATTTCAACTTCTGATTTGACAGACATGTT 1380
DB 1321 TGACGCATATCATCTCATCATCATCTTGATTTCAACTTCTGATTTGACAGACATGTT 1380
QY 1381 GCTGATCAGTAAACGTTGCCGTTGTAATGTTGCTTATCAGGTGTTCAACCTGG 1436
DB 1381 GCTGATCAGTAAACGTTGCCGTTGTAATGTTGCTTATCAGGTGTTCAACCTGG 1436

RESULT 2
AAA27333
ID AAA27333 standard; DNA; 3003 BP.
XX
AC AAA27333;
XX
DT 10-AUG-2000 (first entry)
XX
DE Rice RA8 anther-specific gene.
XX
KW RA8; rice; anther-specific; self-pollination; antisense; transgene;
KW transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor;
KW male-sterile plant; ds.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers

FT exon 1..1288
FT /tag= e
FT /number= 1
FT promoter 1..1196
FT /tag= a
FT CAAT_signal 1116..1119
FT /tag= b
FT TATA_signal 1145..1151
FT /tag= c
FT CDS 1247..2769
FT /tag= d
FT /product= "RA8"
FT /note= "Contains 2 introns"
FT intron 1289..1422
FT /tag= f
FT /number= 1
FT exon 1423..1555
FT /tag= g
FT /number= 2
FT intron 1556..2149
FT /tag= h
FT /number= 2
FT exon 2150..3003
FT /tag= i
FT /number= 3
XX WO200026389-A2.
XX 11-MAY-2000.
XX 02-NOV-1999; 99WO-EP008360.
XX 03-NOV-1998; 98KR-00046973.
XX 19-NOV-1998; 98KR-00050126.
XX (NOVS) NOVARTIS AG.
XX (NOVS) NOVARTIS-ERFINDUNGEN VERM GES MBH.
PI An G, Jeon J, Chung Y, Lee S;
XX WPI; 2000-365632/31.
DR P-PSDB; AAY96273.
XX Novel promoters of anther-specific transcription used to create
PT transgenic male-sterile plants.
XX
PS Claim 3; Page 27-28; 32pp; English.
XX
CC The present sequence is the gene for the rice RA8 protein. This protein
CC is expressed in an anther-specific manner in the plant, where it aids in
CC the development of the structure. The gene can be used to create
CC transgenic plants which do not possess a properly formed anther, and thus
CC are male-sterile. This is useful as it prevents self-pollination, which
CC will then aid breeding and hybrid seed production. In addition to rice,
CC this process can also be used in wheat, maize, orchardgrass and Sorghum
CC bicolor
XX
SQ Sequence 3003 BP; 736 A; 747 C; 694 G; 826 T; 0 U; 0 Other;

Query Match 100.0%; Score 1436; DB 3; Length 3003;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1436; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATTCAGATCATCTCCAGCCTACATGTAATCTCCCATATATACAGTGTCTATGA 60
Db 1 CATTCAGATCATCTCCAGCCTACATGTAATCTCCCATATATACAGTGTCTATGA 60
QY 61 TTCAAAATTTGTCTACATAATAACATTTCCAGCATGAAATCCATACATTATTTTCA 120
Db 61 TTCAAAATTTGTCTACATAATAACATTTCCAGCATGAAATCCATACATTATTTTCA 120
QY 121 CTAATCAGATGCTTGAGGAGAAATCTAAGCGATTCAATATGCAAAATTGATCACTGA 180
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Db 121 CTAATCAGATGCTTGAGGAGAAATCTAAGCGATTCAATATGCAAAATTGATCACTGA 180
QY 181 AGTACTGAAAGAGATATCTCGTTTAAACATTAAGTCTAGTATTTATTAACAATAAA 240
Db 181 AGTACTGAAAGAGATATCTCGTTTAAACATTAAGTCTAGTATTTATTAACAATAAA 240
QY 241 AAATGTTATATTTTAACTACAAATCGAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG 300
Db 241 AAATGTTATATTTTAACTACAAATCGAGTAGTAGCAGTAGCAGAGCTAGCGTAAGATCG 300
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Db 301 TGTTCGATCACCTGAGAAACCGTCAGGTGTTGTCTGTGCCGTCAGCGCATCAGAAAT 360
QY 361 TCGAGATCCGCCGTGTTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAGCAG 420
Db 361 TCGAGATCCGCCGTGTTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAGCAG 420
QY 421 AGCAAGAGCAATGGCGTGCAGGAGTTGAATCTTGATGCACTAGCTAAGTAGCGG 480
Db 421 AGCAAGAGCAATGGCGTGCAGGAGTTGAATCTTGATGCACTAGCTAAGTAGCGG 480
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Db 601 AAATTATGAAGACAGCTGCTGAGAACTAGCTGTGAGAAATCGAAGAAATTGAGTTCT 660
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Db 661 ACGTTCATTCGCAATTTCTACATTAAGATTTCTTATATTTAGTAAAGAGCTGACT 720
QY 721 GTTGGAGCTTCTGTACAGCCGAGATTCTGTGAGAAAGCTGCAGCTGCTGAGAACTTCCC 780
Db 721 GTTGGAGCTTCTGTACAGCCGAGATTCTGTGAGAAAGCTGCAGCTGCTGAGAACTTCCC 780
QY 781 CAAACAGACCCCTAGTTGTACTGTAGCTGATCGATTCACTCTATTTATATACACCTGCG 840
Db 781 CAAACAGACCCCTAGTTGTACTGTAGCTGATCGATTCACTCTATTTATATACACCTGCG 840
QY 841 TCTTAGCTTATCAAAAGTAGCCAAAGCTGAATTTTAAAGCTTAAATTTGATTTGATGT 900
Db 841 TCTTAGCTTATCAAAAGTAGCCAAAGCTGAATTTTAAAGCTTAAATTTGATTTGATGT 900
QY 901 TCTTTTCAATGTAATTTCACTTACCGACCTTAGTCGGCATTTGAATTTTAAATAATATT 960
Db 901 TCTTTTCAATGTAATTTCACTTACCGACCTTAGTCGGCATTTGAATTTTAAATAATATT 960
QY 961 TTAGAGCTGATTTTGATTTTCTTACGGGAAATTTATTTTACCGTATGTAAAGTTTA 1020
Db 961 TTAGAGCTGATTTTGATTTTCTTACGGGAAATTTATTTTACCGTATGTAAAGTTTA 1020
QY 1021 CCTATAAATTAATTTTACGGGAGTAAGCAATTAGTTATGGTTAATATCATCTGG 1080
Db 1021 CCTATAAATTAATTTTACGGGAGTAAGCAATTAGTTATGGTTAATATCATCTGG 1080
QY 1081 TATGCTTAAATCTCTTACTTGAGCTTAGTGGAACAATTCGTAATGCAATTCCTGCGCA 1140
Db 1081 TATGCTTAAATCTCTTACTTGAGCTTAGTGGAACAATTCGTAATGCAATTCCTGCGCA 1140
QY 1141 TCTCTATAATACGGCCTGCTAGCTTTGCTTGATCTGCACAGAACTAGCTGCGAA 1200
Db 1141 TCTCTATAATACGGCCTGCTAGCTTTGCTTGATCTGCACAGAACTAGCTGCGAA 1200
QY 1201 AGTCCTCAAGGGAACCGCCTCCATCTTCTCTTCCAGCTCTCCCATGGCGTCCCTCGT 1260
Db 1201 AGTCCTCAAGGGAACCGCCTCCATCTTCTCTTCCAGCTCTCTCCCATGGCGTCCCTCGT 1260

OY	1261	CGCCATGCGCCATGCCCATGGCTCTCATGTGCAGAGATATCCAGCATGCTGAATTAACT	1320
Dp	1261	CGCCATGCGCCATGCCATGGCTCTCATGTGCAGAGATATCCAGCATGCTGAATTAACT	1320
OY	1321	TGACGCATATCATCTCATTCATCACTTGCACTTCTGATTGTGCAGACAATTTTA	1380
Dp	1321	TGACGCATATCATCTCATTCATCACTTGCACTTCTGATTGTGCAGACAATTTTA	1380
OY	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTGGTCCCTTATCAGGTGGTTCAACCCTGG	1436
Dp	1381	GCTGATCAGTAAACGTTGCCGTGTGAATTGGTCCCTTATCAGGTGGTTCAACCCTGG	1436

```

RESULT 3
AAA27335
ID      AAA27335 standard; DNA; 1196 BP.

```

AC AAA27335;

DT 10-AUG-2000 (first entry)

Rice Ra8 anther-specific gene promoter.

KW RA8; rice; anther-specific; self-pollination; antisense; transgene;
KW transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor;
KW male-sterile plant; ds.

Oryza sativa.

PN WO200026389-A2.

PD 11-MAY-2000.

PF 02-NOV-1999; 99WO-EP008360.

03-NOV-1998; 98KR-00046973.

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466
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PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

PI An G, Jeon J, Chung Y, Lee S;

DR WPI; 2000-365632/31.

Novel promoters of anther-specific transcription used to create transgenic male-sterile plants.

PS Claim 9; Page 29; 32pp; English.

The present sequence is the gene promoter for the rice R8 protein. This protein is expressed in an anther-specific manner in the plant, where it aids in the development of the structure. The gene can be used to create transgenic plants which do not possess a properly formed anther, and thus are male-sterile. This is useful as it prevents self-pollination, which will then aid breeding and hybrid seed production. In addition to rice, this process can also be used in wheat, maize, orchardgrass and Sorghum bicolor

Sequence 1196 BP; 336 A; 242 C; 224 G; 394 T; 0 U; 0 Other;

Query Match	83.3%	Score 1196;	DB 3;	Length 1196;
Best Local Similarity	100.0%	Pred. No. 8.9e-290;		
Matches 1196;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db
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QY 61 TTCAAAATTTGTCTACATATAAACATTTCCAGCATGAATCCATACATTAAATTTTCAG 120
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Db 61 TTCAAAATTTGTCTACATATAAACATTTCCAGCATGAATCCATACATTAAATTTTCAG 120
|||||

OY
121 CTAATCAGATGCTTGAGGGAAAAA TCTAA GCGATTCAATATGC AAAAATTGATCACTGA 180

Dδ
121 CTAATCAGATGCTTGAGGGAAAAA TCTAA GCGATTCAATATGC AAAAATTGATCACTGA 180

Oy	181	AGTAACTGAAGAGATACTCGTTTAA	CA	TTAGTGTCTAGTATTATTAA	CAACTAAA	240
Db	181	AGTAACTGAAGAGATACTCGTTTAA	CA	TTAGTGTCTAGTATTATTAA	CAACTAAA	240

Ox	241	AAATGTTTATTATTAGTACAAATCGAGTAGCAGTGACGTACGCTTAAGATCG	300
Db	241	AAATGTTTATTATTAGTACAAATCGAGTAGCAGTGACGTACGCTTAAGATCG	300

Ox		301 TGTTCGATCACCCTGAAGAACCCGTCAAGTGGTTTGTCGTGTGCCCGTCCAAGCCGATCAGAAT	360
Dδ		301 TGTTCCGATCACCTGAGAAACCCGTCAAGTGGTTTTGTCTGTGTGCCCGTCCAAGCCGATCAGAAT	360

Oy	361	TCGAGATCCGCCGTCGTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAG	420
Db	361	TCGAGATCCGCCGTCGTTCTTCTGAAATCTGCAAGTCCAGCAGCAGCAGCAG	420

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Ox      421 AGCAAGACGAATGGCGGTGCAGGAGTTTGATACTTGTATGCATTAGCTACTAAGGCC   480  
        |||||  
Db     421 ACAGAACAATGGCGGTGCAGGAGTTTGATACTTGTATGCATTAGCTACTAAGGCC   480
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QY	481	TTTCGTTCCATGTGCTCTCAGCCCGTGGGAATGTGCCATGATCTGCATGCATCATCGCC	540
Db	481	TTTCGTTCCATGTGCTCTCAGCCCGTGGGAATGTGCCATGATCTGCATGCATCATCGCC	540

Oy 541 AAGATTATATTCCTCACATTTTTCCTTCTATCGCTCCTAGTCGTCGTGGAGCTTAA 600
 |||||
 Db 541 AAGATTATATTCCTCACATTTTTCCTTCTATCGCTCCTAGTCGTCGTGGAGCTTAA 600

QY 601 AATTTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGATCTGAAGAAATTGAGTTCT 660
|||||
Db 601 AATTTATGAAAGCAGCTGCTGAGAAGCTAGCTGGTGAGATCTGAAGAAATTGAGTTCT 660

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QY      661  ACGTTCATTCTCCAGATTCTACAATTACAGATTCCTATAATTTAGGTAAGGTAAGCTGGACT   720
        |||||
Db      661  ACGTTCATTCTCCAGATTCTACAATTACAGATTCCTATAATTTAGGTAAGGTAAGCTGGACT   720

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QY 721 GTTGGGAGCTTCTGTCA GCCCGAGATTCTGTGAGAA GCTGCAGCTGTCTAGAA GCTTCCC 780

Db 721 GTTGGGAGCTTCTGTCA GCCCGAGATTCTGTGAGAA GCTGCAGCTGTCTAGAA GCTTCCC 780

QY 781 CAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCACTCTATTTTATATACACCTTGC 840

Db 781 CAACAGACCCCTAGTTGTACTCTAGCTGATCGATTCACTCTATTTTATATACACCTTGC 840

[illegible][illegible]

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QY      961 TTAGAGCTGATTTTGATTTTTTTTCAGCGGAATTATTTTCACGATGTAAAGTTT 102
      |||
      961 TTAGAGCTGATTTTGATTTTTTTTCAGCGGAATTATTTTCACGATGTAAAGTTT 102
Db

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Qy	1021	CCATAAATTATTAATTTTCAGCGAGTAAAGCATTAGTGTTATGGGTATTAATCATCTGG	108
Db	1021	CCATAAATTATTAATTTTCAGCGAGTAAAGCATTAGTGTTATGGGTATTAATCATCTGG	108

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Qy      1081 TATGCTAAATCTCTTACTTGACCTAGTTGGACAATTGTAATGCATTCGTGCCA 114
        |||||
Db      1081 TAGCTAAATCTCTTACTTGACCTAGTTGGACAATTGTAATGCATTCGTGCCA 114
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Qy	1141	TCTATATAATACGGCCTGCTAGCTTGTCTCTGTATCTGCACACAGAAGTACGCTG	1196
Db	1141	TCTATATAATACGGCCTGCTAGCTTGTCTCTGTATCTGCACACAGAAGTACGCTG	1196

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RESULT 4
AAA27341
ID AAA27341 standard; DNA; 240 BP.
XX
AC AAA27341;
XX
DT 10-AUG-2000 (first entry)
XX
DE Rice RA8 anther-specific gene fragment.
XX
KW RA8; rice; anther-specific; self-pollination; antisense; transgene;
KW transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor;
KW male-sterile plant; ds.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT exon 1..92
FT /tag= b
FT /number= 1
FT CDS 51..240
FT /tag= a
FT /product= "RA8"
FT /note= "Contains an intron"
FT intron 93..226
FT /tag= c
FT /number= 1
FT exon 227..240
FT /tag= d
FT /number= 2
XX
PN WO200026389-A2.
XX
PD 11-MAY-2000.
XX
PF 02-NOV-1999; 99WO-BP008360.
XX
PR 03-NOV-1998; 98KR-00046973.
PR 19-NOV-1998; 98KR-00050126.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI An G, Jeon J, Chung Y, Lee S;
XX
DR WPI; 2000-365632/31.
DR P-PSDB; AAY96273.
XX
PT Novel promoters of anther-specific transcription used to create
PT transgenic male-sterile plants.
XX
PS Claim 13; Page 32; 32pp; English.
XX
CC The present sequence is part of the gene for the rice RA8 protein. This
CC protein is expressed in an anther-specific manner in the plant, where it
CC aids in the development of the structure. The gene can be used to create
CC transgenic plants which do not possess a properly formed anther, and thus
CC are male-sterile. This is useful as it prevents self-pollination, which
CC will then aid breeding and hybrid seed production. In addition to rice,
CC this process can also be used in wheat, maize, orchardgrass and Sorghum
CC bicolor. This sequence was used to create an expression vector for the
CC protein
XX
SQ Sequence 240 BP; 51 A; 71 C; 49 G; 69 T; 0 U; 0 Other;
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Query Match 16.7%; Score 240; DB 3; Length 240;
Best Local Similarity 100.0%; Pred. No. 4.6e-50;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1197 GCAAAGTCTCAAGGCGAACCCTCCATCTTCTCTTCAGCTCCTCCCAAGCGCTCCC 1256
Db 1 GCAAAGTCTCAAGGCGAACCCTCCATCTTCTCTTCAGCTCCTCCCAAGCGCTCCC 60
```

```
QY 1257 TCGTGGCCATGCCCATGCCCATGGCTTCTCATGGTGACAGATATCCAGATGCTGAATT 1316
Db 61 TCGTGGCCATGCCCATGCCCATGGCTTCTCATGGTGACAGATATCCAGATGCTGAATT 120
QY 1317 AACTGACGCAATCATCTTCATCATCACTTGCACTTCAACTTCTGATGTCAGACATG 1376
Db 121 AACTGACGCAATCATCTTCATCATCACTTGCACTTCAACTTCTGATGTCAGACATG 180
QY 1377 TTTAGCTGATCAATTAACGTTGCCGTGTGAATTGGTCTTATCAGGTGTTCAACTGG 1436
Db 181 TTTAGCTGATCAATTAACGTTGCCGTGTGAATTGGTCTTATCAGGTGTTCAACTGG 240
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```
RESULT 5
AAA27338
ID AAA27338 standard; cDNA; 1008 BP.
XX
AC AAA27338;
XX
DT 10-AUG-2000 (first entry)
XX
DE Rice RA8 anther-specific gene.
XX
KW RA8; rice; anther-specific; self-pollination; antisense; transgene;
KW transgenic plant; wheat; maize; orchardgrass; Sorghum bicolor;
KW male-sterile plant; ss.
XX
OS Oryza sativa.
XX
FH Key Location/Qualifiers
FT CDS 51..845
FT /tag= a
FT /product= "RA8"
XX
PN WO200026389-A2.
XX
PD 11-MAY-2000.
XX
PF 02-NOV-1999; 99WO-BP008360.
XX
PR 03-NOV-1998; 98KR-00046973.
PR 19-NOV-1998; 98KR-00050126.
XX
PA (NOVS ) NOVARTIS AG.
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI An G, Jeon J, Chung Y, Lee S;
XX
DR WPI; 2000-365632/31.
DR P-PSDB; AAY96273.
XX
PT Novel promoters of anther-specific transcription used to create
PT transgenic male-sterile plants.
XX
PS Claim 19; Page 31; 32pp; English.
XX
CC The present sequence is the gene for the rice RA8 protein. This protein
CC is expressed in an anther-specific manner in the plant, where it aids in
CC the development of the structure. The gene can be used to create
CC transgenic plants which do not possess a properly formed anther, and thus
CC are male-sterile. This is useful as it prevents self-pollination, which
CC will then aid breeding and hybrid seed production. In addition to rice,
CC this process can also be used in wheat, maize, orchardgrass and Sorghum
CC bicolor
XX
SQ Sequence 1008 BP; 145 A; 360 C; 325 G; 178 T; 0 U; 0 Other;
```

```
Query Match 6.6%; Score 95; DB 3; Length 1008;
Best Local Similarity 100.0%; Pred. No. 2e-13;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 1197 GCAAAGTCTCAAGGCGAACCCTCCATCTTCTCTTCAGCTCCTCCATGCGCTCCC 1256
```


Db 1 GCAAGTCTCAAGGCGAACCCTCCATCTTCTTCCAGCTCCTCCATGGCGTCCC 60
OY 1257 TCGTGGCCATCGCCATCGCCATGGCTCTCATGTG 1291
Db 61 TCGTGGCCATCGCCATCGCCATGGCTCTCATGTG 95

RESULT 6
ADA71441
ID ADA71441 standard; DNA; 2000 BP.

XX ADA71441;
AC
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 4764.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KM Gene; ds.

OS Oryza sativa.

PN MO2003000898-A1.

PD 03-JAN-2003.

PF 22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

DR WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

PS Claim 27; SEQ ID NO 4764; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.

XX Sequence 2000 BP; 630 A; 343 C; 386 G; 640 T; 0 U; 1 Other;

Query Match 6.3%; Score 90.4; DB 8; Length 2000;
Best Local Similarity 71.1%; Pred. No. 3.8e-12;
Matches 155; Conservative 0; Mismatches 46; Indels 17; Gaps 2;

OY 593 GGAGCTTAAATATGAAAGCAGCTGTGAGAGCTAGCTGTGAGAACTGAAGATT 652

Db 1686 GGAGCTTAAGATTCTGAGAAACAAGCTAAGAGCTAGCTGTGAGAACTGGAAGC 1745

OY 653 TGAGTTCTAC-----GTTCAATCTCCAGATTCTACAATACAGATTCTTA 697

Db 1746 TGGAAAAACCCAGCTTCTGTCTTCTAGTTCATTTCAGATTCTACATCTATAGATTCTTA 1805

OY 698 TAATTTAGTAAAAAGCTGGAAGCTTTGG--GAGCTTCTGTACAGCCGAGAGATTCTGTGAG 755

Db 1806 GAATCTTGTAAGAAAGATGGGTGTAGGAGAGCTTTGTAGCTAAGATATAGAG 1865

OY 756 AAGCTGAGCTGCTAGAGCTTCCCAACAGACCCCT 793
Db 1866 AAGATGCACTGCTAAAAACTCTTTAAATAGTCTT 1903

RESULT 7
ADJ41616
ID ADJ41616 standard; cDNA; 2000 BP.

XX ADJ41616;

DT 06-MAY-2004 (first entry)

DE Plant cDNA #2616.

XX Plant; gene; ss; transcription; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 26-SEP-2001; 2001US-0325448P.

PR 04-APR-2002; 2002US-0370620P.

XX (BUDW/) BUDWORTH P.

PA (MOUG/) MOUGHAMER T.

PA (BRIG/) BRIGGS S P.

PA (COOP/) COOPER B.

PA (GLAZ/) GLAZEBROOK J.

PA (GOFF/) GOFF S A.

PA (KATA/) KATAGIRI F.

PA (KREP/) KREPS J.

PA (PROV/) PROVART N.

PA (RICK/) RICHE D.

PA (ZHUT/) ZHU T.

XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;

PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;

DR WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 1; SEQ ID NO 2616; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,

CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

Sequence 2000 BP; 628 A; 343 C; 387 G; 641 T; 0 U; 1 Other;

Query Match 6.3%; Score 90.4; DB 12; Length 2000;
Best Local Similarity 71.1%; Pred. No. 3.8e-12;
Matches 155; Conservative 0; Mismatches 46; Indels 17; Gaps 2;

OY 593 GGAGCTTAAATTATGAAAGCAGCTGTGAGAGCTAGCTGTGAGAAATCTGAAGAATT 652
Db 1688 GGAGCTTAAGATTCTGAGAGCAACTGCTAAGAGCTAGCTGTGAGAAATCTGAGAAAGC 1747
OY 653 TGAAGTTCTAC-----GTCATCTCCAGATTCTACAATTACAGATTCTTA 697
Db 1748 TGGAAAACCCAGCTTCTGTCTTCTAGTTCAATTTCCAGATTCTACATCTATAGATTCTTA 1807
OY 698 TAATTAGTAAAGAGCTGGAGCTGTTGG--GAGCTTCTGTACGCCGAGATTCTGTGAG 755
Db 1808 GAATCTGTAAAGAGTGGGTGTAGGGAGAGCTTTTGGTAGCTAGAGATTATAGAGAG 1867
OY 756 AAGCTGCAGCTGTGAGAGCTTCCCAACAGACCCCT 793
Db 1868 AAGATGCAACTGCTAAAAACTCCTTTAATAGTCTT 1905

RESULT 8
AAD38802
ID AAD38802 standard; DNA; 17953 BP.

XX AAD38802;

DT 23-SEP-2002 (first entry)

DE Rice RGA8 contig.30Nippon DNA.

KM Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene;
KM AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding;
KM resistance; agricultural; horticultural; plant protectant; ds.

OS Oryza sativa.

PN WO200234927-A2.

PD 02-MAY-2002.

PF 19-OCT-2001; 2001WO-US046331.

PR 20-OCT-2000; 2000US-0242313P.

PR 09-JUL-2001; 2001US-0303897P.

PA (WISC) WISCONSIN ALUMNI RES FOUND.
PA (USDA) US DEPT OF AGRICULTURE.

PI Leong SA, Farman ML, Chauhan RS, Durfee TJ;

DR WPI; 2002-471442/50.

-PT New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar
PT CO39 useful for conferring or improving resistance of plants to strains
PT of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-
PT CO39.

XX Example 2; Page 59-68; 175pp; English.

CC The invention relates to a polynucleotide isolated from chromosome 11 of
CC Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
CC one or more genes that confer resistance to strains of Magnaporthe grisea
CC having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are
CC useful for conferring or improving resistance of plants to strains of the
CC rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-

CC CO39(t) nucleic acids may be used as probes to detect the presence of
CC and/or expression of Pi-CO39(t) genes, and to produce large quantities of
CC pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful
CC in producing polyclonal or monoclonal antibodies useful as sensitive
CC detection reagents for the presence and accumulation of Pi-CO39(t)
CC polypeptides. The transgenic plants are useful for plant breeding or
CC directly in agricultural or horticultural applications. The present
CC sequence is rice RGA8 contig.30Nippon DNA. This sequence comprises
CC portion of BAC clone 82N20 from Nipponbare, containing RGA8 sequence and
CC ORF NBR7
XX

Sequence 17953 BP; 5074 A; 3615 C; 3742 G; 5522 T; 0 U; 0 Other;

Query Match 5.4%; Score 77.2; DB 6; Length 17953;
Best Local Similarity 68.3%; Pred. No. 1.8e-08;
Matches 142; Conservative 0; Mismatches 53; Indels 13; Gaps 2;

OY 589 TTGGGAGCTTAAATTATGAAAAGCAGCTGTGAGAGCTAGCTGTGAGAAATCTGAAG 648
Db 17088 TTGGGAGCTTAAAGATTCTGAGAGTACTGTGTGAGTACTGATTAATCTGAA 17147
OY 649 AATTGAGTTTACGTTCAATCTCCAGATTCTACAATTACAGATTCTTAATTAGTA 708
Db 17148 AAGTTGGTTT---TTCAACTCTGGCTTCTATACTACAGATTCTTAGAACCTGAGTG 17203
OY 709 AAAAGCTGAGCTGTTTGGAGCTTCTGACCCGAGATTCTGTGAGAACTGCAGCTGC 768
Db 17204 AGATGTAGACTAATTGAGG-----AGCTGGAATTCTTAAAGAACTGCATAATAC 17254
OY 769 TAGAGCTTCCCCAAGACAGACCCCTAGT 796
Db 17255 TAGAAGCTCACTCAAAACAGGGCCTTAGT 17282

RESULT 9

ADA72788/c
ID ADA72788 standard; DNA; 2000 BP.

AC ADA72788;

DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 6113.

KM Plant; bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.

OS Oryza sativa.

PN WO2003000898-A1.

PD 03-JAN-2003.

PF 22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

PS Claim 27; SEQ ID NO 6113; 899pp; English.

CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1

XX	Sequence	2000 BP;	653 A;	376 C;	363 G;	607 T;	0 U;	1 Other;
Query Match		4.2%;	Score 60.4;	DB 8;	Length 2000;			
Best Local Similarity		62.5%;	Pred. No. 0.00013;					
Matches 115;	Conservative	0;	Mismatches 61;	Indels 8;	Gaps 1;			
QY	608	GAAGAAGAGCTGCTGAGAGCTAGCTGCTGAGATCTGAAGAATTGAGTTCTACGTTCA	667					
DB	200	GTAACCCAGTTTCTGAGAACTCGATAAGCTGGGTTTCCAGTTTCTGCTTCTAGTTCA	259					
QY	668	TTCTCCAGATTCTACAATTACAGATTCTTATATATTAGTAAAGCTGGACTGTTGGG	727					
DB	260	TTTCTGATTCTACAACATAAATTCTTAGAATCTGAACCAAAAGCTAAATTGTTGGG	319					
QY	728	AGCTTCTGTGAGCCGAGATTCTGTGAGAAGCTGCAGCTGCTAGAGCTTCCCAACAG	787					
DB	320	ATAGTTTCT-----GATTATGGAGAAGCTGCAGCAGCTAAAAACTCTTCCAAACAG	371					
QY	788	ACCC	791					
DB	372	GCCC	375					

RESULT 12
ADA73357/c
ID ADA73357 standard; DNA; 2000 BP.

AC ADA73357;

DT 20-NOV-2003 (first entry)

DE Rice gene, SEQ ID 6683.

KM Plant; bacterial infection; fungal infection; viral infection; rice;
KM gene; ds.

OS *Oryza sativa.*

PN WO2003000898-A1.

PD 03-JAN-2003.

PF 22-JUN-2001; 2001WO-IB001105.

PR 22-JUN-2001; 2001WO-IB001105.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitlam S, Xie Z, Zhu T, Zou G;

DR WPI; 2003-175290/17.

PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.

PS Claim 27; SEQ ID NO 6683; 899pp; English.

The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.

SQ Sequence 2000 BP; 618 A; 438 C; 283 G; 660 T; 0 U; 1 Other;

Query Match	4.1%	Score 59.2;	DB 8;	Length 2000;
Best Local Similarity	63.8%	Pred. No. 0.00026;		
Matches 134; Conservative	0;	Mismatches 53;	Indels 23;	Gaps 2;

[illegible]

RESULT 13
ADJ40892
ID ADJ40892 standard; cDNA; 2000 BP.

AC ADJ40892;

DT 06-MAY-2004 (first entry)

Plant cDNA #1892.

KM Plant; gene; ss; transcription; plant genome augmentation; cereal;
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;
KM antifungal.

OS Eukaryota.

PN US2004016025-A1.

PD 22-JAN-2004.

PF 26-SEP-2002; 2002US-00260238.

PR 26-SEP-2001; 2001US-0325277P.

PR 04-APR-2002; 2002US-0370620P.

PA (BUDW/) BUDWORTH P.
PA (MOUG/) MOUGHAMER T.
PA (BRIG/) BRIGGS S P.
PA (COOP/) COOPER B.
PA (GLAZ/) GLAZEBROOK J
PA (GOFF/) GOFF S A.
PA (KATA/) KATAGIRI F.
PA (KREP/) KREPS J.
PA (PROV/) PROVANT N.
PA (RICK/) RICHKE D.
PA (ZHUT/) ZHU T.

PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;
PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;
XX
DR WPI; 2004-190374/18.

PT New rice promoter, useful for manipulating crop plants to alter or
PT improve phenotypic characteristics, e.g. produce large quantities of oil
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance
PT or high nutritional value.

PS Claim 33; SEQ ID NO 1892; 230pp; English.

CC The invention relates to plant nucleotide sequences that direct seed-,
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential
CC or constitutive transcription of an operatively linked nucleic acid
CC segment. The invention also relates to a method for augmenting a plant
CC genome and a method of identifying a gene, where its expression is
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they
CC encode are useful for manipulating crop plants to alter or improve
CC phenotypic characteristics, to produce large quantities of oil or
CC proteins, to incur resistance to insecticides, viruses or fungi, and to
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants
CC have a high nutritional value with reduced apical dominance or dwarfism,
CC early flowering or altered metabolic pathways. This sequence represents a
CC plant nucleic acid of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification but was obtained in
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
XX

Query Match	4.1%;	Score 58.8;	DB 12;	Length 2000;
Best Local Similarity	66.5%;	Pred. No. 0.00032;		
Matches 141; Conservative	0;	Mismatches 47;	Indels 24;	Gaps 3;

Oy	589	TTTGGAGCTTAAATTTATGAAAAGCAGCTGCTGAGAAGCTAGCTGTGACAACTCGAAG	648
Db	627	TTGGAGAGCTTAAATTTCTGATTAAGCAACTGATTAGTACCACCT-TTGACAATCTGGAA	685

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Oy      649 AATTGAGTCT-----ACGTTCATCTCCAGATTTACAATTACAGATT   693
        ||| |||||
Db      686 AACCGGGTTTTCTAGTTTTTGACTTCAAGTTCATTTTCTAGATTTCTACAATAACAGTTT   745
```

Qy	694	CTTATTAATTTAGGTAATAAAGCTGGAC	CTGTTTGGAGC	CTTCTGTCA	GCCGAGATT	CTGTG	753
Db	746	CTCAGATCTGGACCAAAAGCTGAC	CTGTTTTAGATAG	TTTTT	-----	GATTCGAT	797

Qy 754 AGAAGCTGCAGCTGCTAGAAAGCTTCCCCCAAC 785
| | | | | | | | | | | | | | | | | | | | | |
Db 798 AGAAGTTGCACACAGCCAAAAGCTCTCCCAAC 829

RESULT 14
AAD38805/c
ID AAD38805 standard; DNA; 11460 BP.

AC AAD38805;

DT 23-SEP-2002 (first entry)

DE CODR1 ORF from rice variety CO39.

KM Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene;
KM AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding;
KM resistance; agricultural; horticultural; plant protectant; ds.

OS *Oryza sativa*.

PN WO200234927-A2.

PD 02-MAY-2002.

PF 19-OCT-2001; 2001WO-US046331.

PR 20-OCT-2000; 2000US-0242313P.

PR 09-JUL-2001; 2001US-0303897P.

PA (WISC) WISCONSIN ALUMNI RES FOUND.
PA (USDA) US DEPT OF AGRICULTURE.

PI Leong SA, Farman ML, Chauhan RS, Durfee TJ;

XX WPI; 2002-471442/50.
DR

PT New Pico39(c) polynucleotides from chromosome 11 of indica rice cultivar
PT CO39 useful for conferring or improving resistance of plants to strains
PT of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-
PT CO39.

PS Claim 6; Page 143-148; 175pp; English.

The invention relates to a polynucleotide isolated from chromosome 11 of *Indica* rice cultivar CO39, flanked by marker R2316 and RG1094 comprising one or more genes that confer resistance to strains of *Magnaporthe grisea* having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are useful for conferring or improving resistance of plants to strains of the rice blast pathogen, *Magnaporthe grisea* and other pathogens. The Pi-CO39(t) nucleic acids may be used as probes to detect the presence of and/or expression of Pi-CO39(t) genes, and to produce large quantities of pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful in producing polyclonal or monoclonal antibodies useful as sensitive detection reagents for the presence and accumulation of Pi-CO39(t) polypeptides. The transgenic plants are useful for plant breeding or directly in agricultural or horticultural applications. The present sequence is CODRI ORF from rice variety CO39

SQ Sequence 11460 BP; 3238 A; 2381 C; 2138 G; 3703 T; 0 U; 0 Other;

Query Match	4.0%;	Score 57.6;	DB 6;	Length 11460;
Best Local Similarity	63.0%;	Pred. No. 0.0013;		
Matches 109; Conservative	0;	Mismatches 56;	Indels 8;	Gaps 1;

```

Oy      638 AGAATCTGAGAAATTGAGTTCTACGTTCAATTCCTCAGATTCTACAATTACAGATTCTTA 697
        |||||
Db      4898 AGCTTCTCCAGCTTCTGCGCTTCTTAGTTCATTTTTCAGATTCTGTAACCTACAGATTCTCA 4839

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QY	698	TAATTAGTAAAGAAGCTGGACTGTTGGAGCCTTCGTACGCCGAGATTCGTGAGAA	757
Db	4838	GAAGCTGTGACTG-----TTTGGGGTAGCCTTCACGACAAGCAGCTTTGGGAAA	4787

QY 758 GCTGACGTGCTAGAGCTTCCCAACAAGACCCTTAGTTGTA CTCTAGCTGA 810
| | | | | | | | | | | | | | | |
Db 4786 GTTACAGCTGGGACCAAGCTCCCCCAAACAGGACCTAAGTTTACACAGTTGGTCA 4734

RESULT 15
AAD38804
ID AAD38804 standard; DNA; 69300 BP.

AC AAD38804;

DT 23-SEP-2002 (first entry)

BAC clone E2P5 from rice variety CO39.

KM Rice; chromosome 11; indica rice cultivar; CO39; avirulence gene;
KM AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding;
KM resistance; agricultural; horticultural; plant protectant; ds.

Oryza sativa.

PN WO200234927-A2.

PD 02-MAY-2002

PF 19-OCT-2001; 2001WO-US046331.

PR 20-OCT-2000; 2000US-0242313P.

PR 09-JUL-2001; 2001US-0303897P.

PA (WISC) WISCONSIN ALUMNI RES FOUND.
PA (USDA) US DEPT OF AGRICULTURE.
PA

PI Leong SA, Farman ML, Chaohan RS, Durfee TJ;

XX WPI; 2002-471442/50.
DR

PT New PiCO39(t) polynucleotides from chromosome 11 of Indica rice cultivar
PT CO39 useful for conferring or improving resistance of plants to strains
PT of Magnaporthe grisea or other plant pathogens with avirulence gene AVR1-
PT CO39.

PS Example 4; Page 110-142; 175pp; English.

CC The invention relates to a polynucleotide isolated from chromosome 11 of
CC Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
CC one or more genes that confer resistance to strains of Magnaporthe grisea
CC having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are
CC useful for conferring or improving resistance of plants to strains of the
CC rice blast pathogen, Magnaporthe grisea and other pathogens. The Pi-
CC CO39(t) nucleic acids may be used as probes to detect the presence of
CC and/or expression of Pi-CO39(t) genes, and to produce large quantities of
CC pure Pi-CO39(t) proteins. Purified gene products of Pi-CO39(t) are useful
CC in producing polyclonal or monoclonal antibodies useful as sensitive
CC detection reagents for the presence and accumulation of Pi-CO39(t)
CC polypeptides. The transgenic plants are useful for plant breeding or
CC directly in agricultural or horticultural applications. The present
CC sequence is BAC clone E2P5 from rice variety CO39

Sequence 69300 BP; 19720 A; 15094 C; 15006 G; 19380 T; 0 U; 100 Other;

Query Match	4.0%	Score 57.6;	DB 6;	Length 69300;
Best Local Similarity	63.0%;	Pred. No. 0.0026;		
Matches 109; Conservative	0;	Mismatches 56;	Indels 8;	Gaps 1;

OY	638	AGATCTGAAGAATTGAGTCTACGTTCA TTC CAGATTCTACAATTACAGATTCTTA	697
Db	12015	AGCTCTCCAGCTTCGGCTTCTTAGTTCATTTTCAGATTCTGTAACTACAGATTCTCA	12074
OY	698	TAATTTAGGTAAAAAGCTGCACTGTTTGAGACTTCTGT CAGCCGAGATTCTGTGAAA	757
Db	12075	GAA GCTGTGACTG-----TTTGGGTTAGCTTCTAGCAGAACAGACTTTTGGGAAA	12126
OY	758	GCTGCAGCTGCTAGAGCTTCCCCAACAAGACCCTAGTTGTA CTAGCTGA	810
Db	12127	GTTACAGCTGGGACAAAGCTCCCCCAAACAGAACCTAAGTTACACAGTTGGTCA	12179

Search completed: September 23, 2005, 17:11:19
Job time : 583 secs

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